

# CLAIMS

1 1. A process for altering the host range of.  
2 Bacillus toxins which comprises recombining in vitro  
3 the variable region of two or more Bacillus toxin genes.

1 2. A process, according to claim 1, wherein the  
2 Bacillus is a Bacillus thuringiensis.

1 3. A process, according to claim 2, wherein  
2 variable regions of Bacillus thuringiensis var.  
3 kurstaki HD-1 and Bacillus thuringiensis var.  
4 kurstaki HD-73 are recombined in vitro to give genes  
5 encoding chimeric toxins having altered host ranges.

1 4. DNA, denoted pEW3, encoding a chimeric toxin  
2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400  
4 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
5 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTTACACCC CAATCGATAT 500  
6 TTCTTGTCTG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG  
7 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
8 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT  
9 AGAAGAATTC GCTAGGAACC AAGCCATTTC TAGATTAGAA GGAATAAGCA 700  
10 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT  
11 ACTAATCCAG CATTAGAGAG AGAGATGCGT ATTCAATTCA ATGACATGAA 800  
12 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG  
13 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
14 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTG ATGCCGCGAC  
15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
16 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
17 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100  
18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
19 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200  
20 GTATTAGAAA ATTTTGATGG TAGTTTTCGA GGCTCGGCTC AGGGCATAGA  
TCTATACGGA TGCTCATAGG GGTTATTATT ATTGGTCAGG GCATCAAATA  
ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCATT TTCCGCTATA 1400  
TGGAAGTATG GGAAATGCAG TTCCACAACA ACGTATTGTT GCTCAACTAG  
GTCAGGGCGT GTATAGAACA CTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
AATATAGGGA TAAATAATCA ACAACTACT GTTCTTGACG GGACAGAATT  
TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA

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21 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTC 1700  
 22 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 (start HD-1) CCAACGT TTTCTTGSCA GCATCGCAGT 1900  
 23 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 24 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000  
 25 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA  
 26 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 27 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
 28 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200  
 29 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA  
 30 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 31 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA  
 32 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 33 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAAACAGAT GTGACGGATT  
 34 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500  
 35 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
 36 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600  
 37 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 38 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 39 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
 40 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 41 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 42 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 43 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 44 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000  
 45 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 46 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 47 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 48 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 49 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 50 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 51 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 52 ATCTGCCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400  
 53 GAATTAGAAG GCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAA  
 54 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGACGTGA 3500  
 55 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT  
 56 CTTCCGGAAT GGGAGGAGAG AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600  
 57 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 58 GTTGCCTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
 59 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 60 TGATTATACT GTAAATCAAG AAGAATACGG AAGTGCCTAC ACTTCTCGTA 3800  
 61 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGTCACTC  
 62 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 63 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 64 AAGAATTAGA ATACTTCCCA GAAACCGATA AAGTATGGAT TGAGATTGGA 4000  
 65 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 66 GGAA (end HD-1)

and equivalent nucleotide sequences coding for toxin  
EW3 with the following amino acid sequence:

MDNNPNINEDCIPYNCLSNPEVEVLGGGERIE  
TGYTPIDISLSLTQFLLSEFVPGAGFVLGL  
VDIIWGI FGPSQWDAFLVQIEQLINQRIEE  
FARNQAI SRLEGLSNLYQIYAESFREWEAD  
PTNPALREEMRIQFNDMNSALTTAIFLFAV  
QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ  
RWGFDAATINSRYNDLTRLIGNYTDYAVRW  
YNTGLERVWGPDSRDWVRYNQFRRELTLTV  
LDIVALLFPNYDSRRYP IRTVSQLTREIYTN  
FVLENFDGSGFRGSAQGIERSIRSPHLM DIL  
NSITITVTD AHRGYY YWSGHQIMASPVGFSG  
PEFTFFPLYGTMGNAAPQQRIVAQLGQGVYR  
TLESSTLYRRPFNIGINNQQLSVLDGTEFAY  
GTSSSNLPSAVYRKSGTVDSDLDEIFPQNNNV  
PFRGGFSSHRLSHVSMFRSGGFSNSSVSIIRA  
PTFSWQHRS AEFNNIIFSSQITQIPLTKST  
NLGSGTSSVVKGPBFTGGDILRRTSPGQIST  
LRVNI TAPLSQRYRVRIRYASTTNLQFHTS  
IDGRFINQGNFSATMSSSGSNLQSGSFRTVG  
FTTFFNF SNGSSSVFTLSAHVFNSGNEVYID  
RIEFVPAEVTFEAEYDLERAQKAVNELFTS  
SNQIGLKT DVTDYHIDQVSNLVECLSD EFC  
LDEKQELSEKVKHAKRLSDERNLLQDPNFR  
GINRQLDRGWRGSTDITIQGGDDVFKENYV  
TLLGT FDECYPTYLYQKIDESK LKAYTRYQ  
LRGYIEDSQDLEIYLIRYN AKHETVNVPGT  
GSLWPLSAQSPIGKCGEPNRCAPHLEWNPD  
LDCSCRDGEEKCAHHSHHFSLDIDVGCTDLN  
EDLGVWVIFKIKTQDGHARLGNLEFLEEK P  
LVGEALARVKRAEKKWRDKREKLEWETNIV  
YKEAKESVDALFVNSQYDQLQADTNIAMIH  
AADKRVHSIREAYLP ELSVIFGVNA AIFEE  
LEGRIFTA FSLYDARNVIKNGDFNNGLS CW  
NVKGHV DVEEQNNQRSVLVLP EWEAEVSQE  
VRVCPGRGYILRV TAYKEGYGEGCVTIHEI  
ENNTDELKFSNCVEEEIYPNNTVTCNDYTV  
NQEEYGGAYTSRNRGYNEAPSVPADYASVY  
EEKSYTDGRRENPCFNRG YRDYTPLPVGY  
VTKELEYFPETDKVWIEIGETEGT FIVDSV  
ELLLMEE.

5. DNA, denoted pEW4, encoding a chimeric toxin,  
having pesticidal activity, as follows:

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      (start HD-1)          ATGG ATAACAATCC GAACATCAAT
1  GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
2  TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
3  TAACGCAATT TCTTTTGAGT GAATTTGTTT CCGGTGCTGG ATTTGTGTTA 700
4  GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
5  ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
6  CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
7  ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
8  ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
9  CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
10 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
11 TTCAGTGTTC GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
12 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
13 CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
14 TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
15 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
16 ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCAG TATTAGAAAA
17 TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
18 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
19 GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
20 TGTAGGGTTT TCAGGACCAG AATTCGCATT CCCTTTATTT GGGAAATGCGG
21 GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
22 AGAACATTAT CTTACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCC
23 AAATAATCAG GAACTGTTT TCCTTGATGG AACGGAGTTT TCTTTTGCCT 1700
24 CCCTAACGAC CAACTTGCC TCCACTATAT ATAGACAAAG GGGTACAGTC
25 GATTCAC TAG ATGTAAATACC GCCACAGGAT AATAGTGAC CACCTCGTGC 1800
26 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
27 GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
      (start HD-73)          CCT ATGTTCTCTT
28 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
29 ACTCAAATCC CTGCAGTGAA GGGAACTTT CTTTTTAATG GTTCTGTAAT
30 TTCAGGACCA GGATTTACTG GTGGGACTT AGTTAGATTA AATAGTAGTG 1900
31 GAAATAACAT TCAGAAATAG AGGTATATTG AAGTTCCAAT TCACTTCCCA
32 TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
33 GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTT TCCAATACAG
34 TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
35 TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
36 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
37 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
38 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
39 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT
40 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
41 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
42 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGBAAGTA 2500
43 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC
44 AACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
45 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT
46 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700
47 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCCTTAT GGCCGCTTTC

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36 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGGCGGCCAC 2800  
 37 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG  
 38 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900  
 39 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC  
 40 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000  
 41 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG  
 42 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100  
 43 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA  
 44 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200  
 45 TAGCATTCTG GAAGCTTATC TGCTGAGCT GTCTGTGATT CCGGGTGTCA  
 46 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300  
 47 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT  
 48 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400  
 49 AACGTTGCGT CCTTGTTGTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA  
 50 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500  
 51 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA  
 CAGACGAACCT GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600  
 AACACGGTAA CGTGAATGA TTATACTGTA AATCAAGAAG AATACGGAGG  
 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700  
 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA  
 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800  
 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG  
 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900  
 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin  
 53 EW4 with the following amino acid sequence:

54 MDNNPNINECIPYNCLSNPEVEVELGGERIE  
55 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL  
56 VDIIWGIFGPSQWDAFPVQIEQLINQRIEE  
57 FARNQAI SRLEGLSNLYQIYAESFREWEAD  
58 PTNFPALREEMRIQFNDMNSALTTAIPLLAV  
59 QNYQVFLLSVYVQAANLHLSVLRDVS VFGQ  
60 RWGFGAATINSRYNDLTRLIGNYTDYAVRW  
61 YNTGLERVWGPDSRDWVRYNQFRRELTTLTV  
62 LDIVALFSSNYDSRRYPPIRTVSQLTREIYTN  
63 PVLLENFDDGSGFRGMAQRIEQNIRQPHLM DIL  
64 NSITIIYTQVHRGFNYWSGHQITASPVGFSG  
65 PEFAPFLFGNAGNAAPPVVLVSLTGLGIFRT  
66 LSSPLYRRIILGSGPNNQELFVLDGTEFSF  
67 ASLTTNLPSTIYRQRTVDSLDVIPQDINS  
68 VPPRAGFSHRLSHVTMLSQAAGAVYTLRAQ  
69 RPFMF SWIHRSAEFNNIIASDSITQIPAVKG  
70 NFLFNGSVISGPGFTGGDLVRLNSSSGNNIQ  
71 NRGYIEVPIHF PSTSTRYRVRYASVTPI  
72 HLN VNWGNSSIFSNTVPATATSLDNLQSSD  
73 FGYFESANAF TSSLGNI VGVNFSGTAGVI  
74 IDRFEFIPVTATLEAEYNLERAQKAVNALF  
75 TSTNQLGLKTNVTDYHIDQVSNLVTYLSDE  
76 FCLDEKRELSEKVKHAKRLSDERNLLQDSN  
77 FKDINRQPERSGWGGSTGITIQGGDDVFKEN  
78 YVTLSGTFDECYPTLYLQKIDESK LKAFTR  
79 YQLRGYIEDSQDLEIYLI RYN AKHETVNV P  
80 GTGSLWPLSAQSPIGKCGEPNRCAPHLEWN  
PDLDCSCRDGEEKCAHHSHHFSLDIDVGCTD  
LNEDLGVWVIFKIKTQDGHARLG NLEFLEE  
KPLVGEALARVKRAEKKWRDKREKLEWETN  
IVYKEAKESVDALFVNSQYDQLQADTNIAM  
IHAADKRVHSIREAYLP ELSVIPGVNA AIF  
EELEGRIFTAFSLYDARNVIKNGDFNNGLS  
QWNVKGHV DVEEQNNQRSVLV VPEWEAEVS  
QEV RVCPGRGYILRV TAYKEGYGEGCVTIH  
EIE NNTDELKFSNCVEEEEIYPNNTVTCNDY  
TVNQE EYGGAYTSRNRGYNEAPSVPADYAS  
VYEEKSYTDGRRENPC EFNRGYRDTPLPV  
GYVTKELEYFPETDKVWIEIGETEGTFIVD  
SVELLLMEE.

1 6. DNA, denoted pACB-1, encoding a chimeric toxin,  
2 having pesticidal activity, as follows:

3 (start HD-73) ATG GATAACAATC 400  
4 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
5 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500  
6 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG  
7 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
8 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT  
9 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700  
10 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT  
11 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCATTCA ATGACATGAA 800  
12 CAGTGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG  
13 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
14 TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC  
15 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
16 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
17 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100  
18 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
19 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200  
20 GTATTAGAAA ATTTTGATGG TAGTTTTGGA GGCTCGGCTC AGGGCATAGA  
21 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
22 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA  
23 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCTT TTCCGCTATA 1400  
24 TGGAACTATG GGAATGCGAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
25 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
26 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
27 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
28 GAACGCTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA  
29 CCTAGGCAAG AATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700  
30 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
31 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900  
32 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
33 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000  
34 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA  
35 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
36 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
37 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200  
38 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA  
39 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA  
41 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
42 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT  
43 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTATATC AGATGAATTT 2500  
44 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
45 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600  
46 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
47 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
48 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
49 TAAAGGCTTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
50 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
51 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
52 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
53 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCGA 3000  
54 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC

55 TAGGTSTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 56 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 58 TGBAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 59 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 60 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 61 ATCTGCCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTTGAA 3400  
 62 GAATTAGAAG GGCATTTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 63 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT  
 65 CTTCCGGAAT GGGGAAGCAGA AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600  
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 67 GTTGCCTAAC CATTATGAG ATCGAGACA ATACAGACGA ACTGAAGTTT 3700  
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 70 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGCTCAGTC  
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 73 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 74 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin  
 77 ACB-1 with the following amino acid sequence:

78 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
 79 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
 80 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
 81 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
 82 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
 83 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
 84 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
 85 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
 86 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
 87 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
 88 N S I T I Y T D A H R G Y Y W S G H Q I M A S P V G F S G  
 89 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
 90 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
 91 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V  
 92 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A  
 93 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
 94 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
 95 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
 96 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G





27 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
 28 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 29 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700  
 30 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 31 (start HD-1) CCAACGT TTTCTTGSCA GCATCGCAGT 1900  
 32 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 33 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCTGT AAAGGACCAG 2000  
 34 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTACCTGG CCAGATTTC  
 35 ACCTTAAGAG TAAATATTAC TGCACCATT TACAAAAGAT ATCGGGTAAG 2100  
 36 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
 37 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200  
 38 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA  
 39 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 40 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAASTA  
 41 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 42 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT  
 43 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500  
 44 TGCTCTGGAG AAAAACAGAG ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
 45 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600  
 46 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 47 GGAGGCGATG ACGTATTCAA AGABAATTAC GTTACGCTAT TGGGTACCTT 2700  
 48 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
 49 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 50 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 51 TGTGCCAGGT ACGGGTTCCT TATGSCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 52 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 53 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000  
 54 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 55 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 56 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 57 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 58 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 59 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 60 TGCCATGATT CATGCGGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 61 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGGAA 3400  
 62 GAATTAGAAG GCGGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 63 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 64 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTTGTT  
 65 CTTCCGGAAT GGGGAAGCAGA AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600  
 66 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 67 GTTGCCTAAC CATTCATGAG ATCAGAGACA ATACAGACGA ACTGAAGTTT 3700  
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 69 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 70 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TCGCTCAGTC  
 71 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 72 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 73 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 74 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 75 GGAA (end HD-1)

76 and equivalent nucleotide sequences coding for toxin  
 77 SYW1 with the following amino acid sequence:

78 MDNNPNINECIPYNCLSNPEVEEVLGGGERIE  
 79 TGYTFIDISLSLTQFLLSSEFVPGAGFVLGL  
 80 VDI IWGIFGPSQWDAFLVQIEQLINQRIEE  
 81 FARNQAISRLEGLSNLYQIYAESFREWEAD  
 82 PTNPALREEMRIQFNDMNSALTTAIPLFAV  
 83 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ  
 84 RWGFDAATINSRYNDLTRLIGNYT DYAVRW  
 85 YNTGLERVWGPDSRDWVRYNQFRRELT LT V  
 86 LDIVALFPNYDSRRYP IRTVSQLTREIYTN  
 87 PVLENFDGSGFRGSAQGI EGSI RSPHLM DIL  
 88 NSIT IYTD AHKG EY YWSGHQIMASPVGFSG  
 89 PEFTTFPLYGT MGN A A PQQRI VAQLGQGVYR  
 90 TLSSTLYRRPFNIGINNQQLSVLDGTEFAY  
 91 GTSSSNLPSAVYRKSGTVDSLDEIPPQNNNV  
 92 PPRQGFSHRLSHVSMFRSGFSNSSVSIIRA  
 93 PTF SWQHRS AEFNNIIPSSQITQIPLTKST  
 94 NLGSGT SVVKGP GFTGGDILRRTSPGQIST  
 95 LRVNITAPLSQRYRVRI RYASTTNLQFHTS  
 96 IDGRPINQGNFSATMSSSGSNLQSGSFRTVG  
 97 FTTFPNFSGSSVFTLSAHVFNSGNEVYID  
 98 RIEFVPAEVTGFEAEYDLERAQKAVNELFTS  
 99 SNQIGLKT DVT DYHIDQVSNLVECLSD EFC  
 100 LDEKQELSEKVKHAKRLSDERNLLQDPNFR  
 101 GINRQLDRGWRGSTDITIQGGDDVFKENYV  
 102 TLLGTFDECYPTYLYQKIDESKLKAYTRYQ  
 103 LRGYIEDSQDLEIYLI RYN AKHETVNVPGT  
 104 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP D  
 105 LDCSCRDGEKCAHHSHHFSLDIDVGCTDLN  
 106 EDLG VWVIFKIKTQDGHARLG NLEFLEEK P  
 107 LVGEALARVKRAEK KWRDKREKLEWETNIV  
 108 YKEAKESVDALFVNSQYDQLQADTNIAMIH  
 109 AADKRVHSIREAYLPELSVIPGVNA AIFEE  
 110 LEGRIFTAFSLYDARNVIKNGDFNNGLS CW  
 111 NVKGHV DVEEQNNQRSVLVLPEWEAEV SQE  
 112 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI  
 113 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV  
 114 NQEEYGGAYT SRNRGYNEAPSVPADYASVY  
 115 EEKSYTDGRRENPCFNRGYRDYTPLPVGY  
 116 VTKELEYFPETDKVWIEIGETEGTFIVDSV  
 117 ELLLMEE.

1 8. A chimeric toxin, EW3, having pesticidal  
2 activity, having the following amino acid sequence:

3 MDNNPNIN ECIPYNC LSNPEVEVLGGERIE  
4 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL  
5 VDIIWGIFGFSQWDAFLVQIEQLINQRIEE  
6 FARNQAI SRLEGLSNLYQIYAESFREWEAD  
7 PTNPALREEMRIQFNDMNSALTTAIFLFAV  
8 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ  
9 RWGFDAATINSRYNDLTRLIGNYT DYAVRW  
10 YNTGLERVWGPDSRDWVRYNQFRRELT LT V  
11 LDIVALFPNYDSRRYP IRTVSQLTREIYTN  
12 PVLENFDGSGFRGSAQGIERSIRSPHLM DIL  
13 NSITIIYTD AHRGYYYWSGHQIMASPVGFSG  
14 PEFTTFPLYGTMGNAAPQQRIVAQLGQGVYR  
15 TLSSTLYRRPFNIGINNQQLSVLDGTEFAY  
16 GTSSSNLPSAVYRKSGTVDSLDEIPPQNNNV  
17 PPRQGFSHRLSHVSMFRSGGFSNSSVSIIRA  
18 PTFSWQHRS AEFNNIIFSSQITQIPLTKST  
19 NLGSGT SVVKGP GFTGGDILRRTSPGQIST  
20 LRVNITAPLSQR YRVRIRYASTTNLQFHTS  
21 IDGRFINQGNFSATMSSSGSNLQSGSFRTVG  
22 FTTPFNF SNGSSSVFTLSAHVFNSGNEVYID  
23 RIEFVPAEVTFEAEYDLERAQKAVNELFTS  
24 SNQIGLKT DVTDYHIDQVSNLVECLSD EFC  
25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR  
26 GINRQLDRGW RGSTDITIQGGDDVFKENYV  
27 TLLGT FDECYPTYLYQK IDESKLKAYTRYQ  
28 LRGYIEDS QDLEIYLIRYN AKHETVNVPGT  
29 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP D  
30 LDCSCR DGEKCAHHSHHFSLDIDVGC TDLN  
31 EDLGVWVIFKIKTQDGHAPLGNLEFLEEK P  
32 LVGEALARVKRAEKKWRDKREKLEWETNIV  
33 YKEAFESVDALFVNSQYDQLQADTNIAMIH  
34 AADKR VH SIREAYLP ELSVIFGVNAAIFEE  
35 LEGRI FTAFSLYDARNV IKNGBDFNNGLS CW  
36 NVKGHV DVEEONNQRSVLVLPEWEAEVSOE  
37 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI  
38 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV  
39 NQEEYGGAYTSRN RGYNEAPSVPADYASVY  
40 EEKSYTDGRRENPC EFNRGYR DYTF LPVGY  
41 VTKELEYFPETDKVWIEIGETEGT FIVDSV  
42 ELLLMEE

43 and muteins thereof which do not alter the protein  
44 secondary structure.

1 9. A chimeric toxin, EW4, having pesticidal  
2 activity, having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E  
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V  
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
11 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N  
12 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L  
13 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G  
14 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T  
15 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F  
16 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S  
17 V F P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q  
18 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G  
18 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q  
20 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I  
21 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D  
22 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I  
23 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F  
24 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E  
25 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N  
26 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N  
27 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R  
28 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P  
29 G T G S L W P L S A Q S P I G K C G E F N R C A P H L E W N  
30 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D  
31 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E  
32 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N  
33 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M  
34 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F  
35 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S  
36 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S  
37 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H  
38 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y  
39 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S  
40 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V  
41 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D  
42 S V E L L L M E E

43 and muteins thereof which do not alter the protein  
44 secondary structure.

-58-

1 10. A chimeric toxin, ACB-1, having pesticidal  
2 activity, having the following amino acid sequence:

3 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G  
14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
16 G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V  
17 P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A  
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
28 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K F  
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E  
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
42 E L L L M E E

43 and muteins thereof which do not alter the protein  
44 secondary structure.

1 11. A chimeric toxin, SYW1, having pesticidal  
2 activity, having the following amino acid sequence:

3 MDNNPNIN ECIPYNCLSNPEVEVELGGERIE  
4 TGYTFIDISLSLTQFLLSEFVPGAGFVLGL  
5 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE  
6 FARNQAISRLEGLSNLYQIYAESFREWEAD  
7 PTNPALREEMRIQFNDMMNSALTTAIPLFAV  
8 QNYQVPLLSVYVQAANLHL SVLRDVSVFGQ  
9 RWGFDAA TINSRYN DLTRLIGNYT DYAVRW  
10 YNTGLERVWGPDSRDWVRYNQFRRELTLTV  
11 LDIVALFPNYDSRRYP IRTVSSQLTREIYT  
12 PVLENFDGGSFRGSAQGGIEGSI RSPHLM  
13 NSITIIYTDAHKGEY YWSGHQIMASPV  
14 PEFTTFPLYGTMGNAAPQQRIVAQLGGVYR  
15 TSSSTLYRRP FNIGINNQLSVLDGTEFAY  
16 GTSSNLP S AVYRKSGT VDSGFSNS SVS  
17 PPRQGFSHRLSHVSMF RSGFSNS SVS  
18 PTFSSWQHRS AEFNNIIPSSQITQIPLTKST  
19 NLGSGT SVVKGPGFTGGDILRRTSPGQIST  
20 LRVNRITAPLSQRYRVRI RYASTTNLQFHTS  
21 IDGRPINQGNFSATMSSSGSNLQSGSFRTVG  
22 FTTPFNF SNGSSSVFTLSAHVFNSGNEVYID  
23 RIEFVPAEVTFEAEYDLERAQKAVNELFTS  
24 SNQIGLKT DVTDYHIDQVSNLVECLSD EFC  
25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR  
26 GINRQLDRGW RGSTDTITIQGGDDVFKENYV  
27 TLLGTFDECYPTYLYQKIDESK LKAYTRYQ  
28 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT  
29 GSLWFLSAQSPIGKCGEPNRCAPHLEWNP  
30 LDCSCR DGEKCAHHS HHFSLDIDVGC TDLN  
31 EDLG V W VIFKIKTQDGHARLG NLEFEEKP  
32 LVGEALARVKRAEKKWRD KREKLEWETNI  
33 YKEAKESVDALFVNSQYDQLQADTNIA MIH  
34 AADKR VHSIREAYLP ELSVIPGVNA AIFEE  
35 LEGRIFTAFSLYDARNV IKN GDFNGLSCW  
36 NVKGHV DVEEQNNQR SVLVLP EWAEV SQE  
37 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI  
38 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV  
39 NQEEYGGAYTSRNRGYNEAPSVPADYASVY  
40 EEKSYTDGRRENPC EFNRGYRDYTPLPVGY  
41 VTKELEYF PETDKVWIEIGETEGTFIVDSV  
42 ELLLMEE

43 and muteins thereof which do not alter the protein  
44 secondary structure.

1           12: A pesticidal composition comprising pesti-  
2       cide-containing substantially intact cells having  
3       prolonged pesticidal activity when applied to the  
4       environment of a target pest, wherein said pesticide,  
5       is a chimeric toxin, is intracellular and is produced  
6       as a result of expression of a heterologous gene  
7       encoding said chimeric toxin in said cell.

1           13. A pesticidal composition according to claim 12,  
2       wherein said cells are killed under protease deacti-  
3       vating or cell wall strengthening conditions, while  
4       retaining pesticidal activity.

1           14. A pesticidal composition, according to claim 12,  
2       wherein said cells are prokaryotes selected from the  
3       group consisting of Enterobacteriaceae, Bacillaceae,  
4       Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-  
5       monadaceae, Azotobacteraceae, and Nitrobacteraceae; or  
6       lower eukaryotes selected from the group consisting  
7       of Phycomycetes, Ascomycetes, and Basidiomycetes.

1           15. A pesticidal composition, according to claim 14,  
2       wherein said prokaryote is a Bacillus specie selected  
3       from a pesticide-producing strain of Bacillus thurin-  
4       giensis, consisting of B. thuringiensis M-7, B. thurin-  
5       giensis var. kurstaki, B. thuringiensis var. finitimus,  
6       B. thuringiensis var. alesti, B. thuringiensis var.  
7       sotto, B. thuringiensis var. dendrolimus, B. thurin-  
8       giensis var. kenyae, B. thuringiensis var. galleriae,  
9       B. thuringiensis var. canadensis, B. thuringiensis var.  
10      entomocidus, B. thuringiensis var. subtoxicus, B.  
11      thuringiensis var. aizawai, B. thuringiensis var. morri-  
12      soni, B. thuringiensis var. ostrinae, B. thuringiensis  
13      var. tolworthi, B. thuringiensis var. darmstadiensis,



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14 B. thuringiensis var. toumanoffi, B. thuringiensis var.  
15 kyushuensis, B. thuringiensis var. thompsoni, B.  
16 thuringiensis var. pakistani, B. thuringiensis var.  
17 israelensis, B. thuringiensis var. indiana, B. thurin-  
18 giensis var. dakota, B. thuringiensis var. tohokuensis,  
19 B. thuringiensis var. kumanotoensis, B. thuringiensis  
20 var. tochigiensis, B. thuringiensis var. colmeri,  
21 B. thuringiensis var. wuhanensis, B. thuringiensis  
22 var. tenebrionis, B. thuringiensis var. thuringiensis,  
23 and other Bacillus species selected from B. cereus, B.  
24 moritai, B. popilliae, B. lentimorbus, and B. sphaericus.

1 16. A method of protecting plants against pests  
2 which comprises applying to said plants an effective  
3 amount of a pesticidal composition comprising pesti-  
4 cide-containing substantially intact unicellular  
5 microorganisms, wherein said pesticide is a chimeric  
6 toxin, is intracellular, and is produced as a result  
7 of expression of a heterologous gene encoding said  
8 chimeric toxin in said microorganism, and said micro-  
9 organism is treated under conditions which prolong  
10 the pesticidal activity when said composition is applied  
11 to the environment of a target pest.

1 17. A method according to claim 16, wherein said  
2 microorganisms are prokaryotes selected from the  
3 group consisting of Enterobacteriaceae, Bacillaceae,  
4 Rhizobiaceae, Spirillaceae, Lactobacillaceae, Pseudo-  
5 monadaceae, Azotobacteraceae, and Nitrobacteraceae; or  
6 lower eukaryotes, selected from the group consisting  
7 of Phycomycetes, Ascomycetes, and Basidiomycetes.

1 18. A method according to claim 16, wherein said  
2 unicellular microorganisms are killed under protease  
3 deactivating or cell wall strengthening conditions,  
4 while retaining pesticidal activity.

1 19. Substantially intact unicellular microorganism  
2 cells containing an intracellular chimeric toxin, which  
3 toxin is a result of expression of a heterologous  
4 gene encoding said chimeric toxin, wherein said cells  
5 are killed under protease deactivating or cell wall  
6 strengthening conditions, while retaining pesticidal  
7 activity when said cell is applied to the environment  
8 of a target pest.

1 20. Cells according to claim 19, wherein said  
2 microorganism is a Pseudomonad and said toxin is  
3 derived from a B. thuringiensis.

1 21. A pesticidal composition, according to claim  
2 12, wherein said gene, denoted pEW3, encoding a  
3 chimeric toxin, is as follows:

4 (start HD-73) ATG GATAACAATC 400  
5 CGAACATCAA TGAATGCATT CTTATAATT GTTTAAGTAA CCCTGAAGTA  
6 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500  
7 TTCCTTGCTG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG  
8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
9 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT  
10 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700  
11 ATCTTTATCA AATTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT  
12 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800  
13 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG  
14 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
15 TTGAGAGATG TTTCAGTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC  
TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACT 1100  
AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200  
GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA

16 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 17 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA  
 18 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400  
 19 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
 20 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
 21 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
 22 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
 23 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 24 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700  
 25 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 26 (start HD-1) CCAACGT TTTCTTGSCA GCATCGCAGT 1900  
 27 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 28 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGCTT AAAGGACCAG 2000  
 29 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTCA  
 30 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 31 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
 32 GAAGACCTAT TAATCAGGGT AATTTTTTCA CAACTATGAG TAGTGGGAGT 2200  
 33 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA  
 34 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 35 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA  
 36 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 37 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAAACAGAT GTGACGGATT  
 38 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500  
 39 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
 40 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600  
 41 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 42 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 43 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAT  
 44 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 45 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 46 TGTGCCAGGT ACGGGTTTCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 47 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 48 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTGCGA 3000  
 49 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 50 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 51 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAAGCGCT  
 52 AGCTCGTGTG AAAAGAGCGG AGAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 53 TGGAAATGGG AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 54 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 55 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 56 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400  
 57 GAATTAGAAG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 58 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 59 AAGGBCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT  
 60 CTTCGGAAT GGGAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600  
 61 TCGTGCGTAT ATCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 62 GTTGCCTAAC CATTCATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
 63 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 64 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 65 ATCGAGGATA TAACGAAGCT CCTTCGCTAC CAGCTGATTA TCGTCAAGT  
 66 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 67 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 68 AAGAATTAGA ATACTTCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 69 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA  
 70 GGAA (end HD-1)

52 and equivalent nucleotide sequences coding for toxin  
53 EW3 with the following amino acid sequence:

54 MDNNPNININECIPYNCLSNPEVEVEVLGGGERIE  
55 TGYTPIDISLSLTQFLLSSEFVPGAGFVLGL  
56 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE  
57 FARNQAI SRLEGLSNLYQIYAESFREWEAD  
58 PTNPALREEMRIQFNDMNSALTTAIPLFAV  
59 QNYQVPLL SVYVQAANLHLSVLRDVS VFGQ  
60 RWGFD AATINSRYNDLTRLIGNYTDYAVRW  
61 YNTGLERVWGPDSRDWVRYNQFRRELTLTV  
62 LDIV ALFPNYDSRRYP IRTVSQLTREIYTN  
63 PVLENFDGSGFRGSAQGIERSIRSPHLMDIL  
64 NSIT IYTD AHRGYYYWSGHQIMASPVGFSG  
65 PEFTFP LYGTMGNAA PQQRIVAQLGGGVYR  
66 T LSSSTLYRRPF FNIGINNQQLSVLDGTEFAY  
67 GTSSSNLPSAVYRKSGTVDSLDEIPPQNNNV  
68 PPRQGFSHRLSHVSMFRSGFSNSSVSIIRA  
69 PTFSWQHRS AEFNNIIPSSQITQIPLTKST  
70 NLGSGT SVVKGP GFTGGDILRRTSPGQIST  
71 LRVNITAPLSQR YRVRIRYASTTNLQFHTS  
72 IDGRPINQGNFSATMSSSGSNLQSGSFRTVG  
73 FTTFFNF SNGSSVFTLSAHVFNSGNEVYID  
74 RIEFVPAEVTFEAEYDLERAQKAVNELFTS  
75 SNQIGLKTDVTDYHIDQVSNLVECLSD EFC  
76 LDEKQELSEKVKHAKRLSDERNLLQDPNFR  
77 GINRQLDRGWRGSTDITIQQGGDDVFKENYV  
78 TLLGTFDECYPTYLYQK IDESKLKAYTRYQ  
79 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT  
80 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP D  
71 LDCSCRDGEEKCAHHSHHFSLDIDVGCTDLN  
72 EDLGVWVIFKIKTQDGHARLGNLEFLEEK P  
73 LVGEALARVKRAEKKWRDKREKLEWETNIV  
74 YKEAKESVDALFVNSQYDQLQADTNIAMIH  
75 AADKR VHSIREAYLPELSVIFGVNA AIFEE  
76 LEGRIFTAFSLYDARNV IKN GDFNNGLS CW  
77 NVKGHV DVEEQNNQRSVLVLFEWEAEVSQE  
78 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI  
79 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV  
80 NQEEYGGAYTSRNRGYNEAPSVPADYASVY  
81 EEKSYTDGRRENPCFENRGYRDYTPLPVGY  
82 VTKELEYFPETDKVWIEIGETEGTFIVDSV  
83 ELLLMEE.

1           22. A pesticidal composition, according to claim  
2           12, wherein said gene, denoted pEW4, encoding a  
3           chimeric toxin, is as follows:

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4           (start HD-1)                   ATGG ATAACAATCC GAACATCAAT
5           GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
6           TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
7           TAACGCAATT TCTTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
8           GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
9           ATTTCTGTG CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
10           CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
11           ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
12           ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
13           CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
14           TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
15           TTCAGTGTTC GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
16           GTTATAATGA TTTAACTAGG CTTATTGSCA ACTATACAGA TTATGCTGTG
17           CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
18           TTGGGTAAAG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
19           ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGSTA TCCAATTCGA 1300
20           ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
21           TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
22           GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
23           GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
24           TGTAGGGTTT TCAGGACCAG AATTCGCATT CCCTTTATTT GGGGAATGCGG
25           GGAATGCAGC TCCACCCGTA TTGTCTCAT TAAC TGTTT 1600
26           AGAACATTAT CTTACCTTTT ATTAGAAGA ATTATACTTG GTTCAGGCCC
27           AAATAATCAG GAAGTGTG TGCTTGATGG AACGGAGTTT TCTTTTGCCCT 1700
28           CCCTAACGAC CAAGTTGCCT TCCACTATAT ATAGACAAAG GGGTACAGTC
29           GATTCAGTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
30           GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
31           GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
32           (start HD-73)                   CCT ATGTTCTCTT
33           GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
34           ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
35           TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
36           GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
37           TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
38           GATTCACCTC AACGTTAATT GGGGTAATTC ATCCATTTT TCCAATACAG
39           TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
40           TATTTTGAAA GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
41           TGTTAGAAAT TTAGTGGBGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
42           TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

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30 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300  
 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT  
 31 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400  
 GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC  
 32 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCAGGAGTA 2500  
 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAAGA AAATTACGTC  
 33 ACCTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600  
 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT  
 34 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCG CTACAATGCA 2700  
 35 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC  
 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGCCAC 2800  
 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG  
 36 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900  
 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC  
 37 AAGATGGGCA CGCAAGACTA GGAATCTAG AGTTTCTCGA AGAGAAACCA 3000  
 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG  
 38 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100  
 40 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA  
 41 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200  
 TAGCATTCGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA  
 42 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300  
 43 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT  
 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400  
 44 AACGTTGCGT CCTTGTGTT CCGGAATGGG AAGCAGAAAT GTCACAAGAA  
 45 GTTCGTGTCT GTCCGGGTCG TGGCTATATC CTTCTGTGCA CAGCGTACAA 3500  
 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA  
 46 CAGACGAAT GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAT 3600  
 47 AACACGGTAA CGTGTAAATG TTATACTGTA AATCAAGAAG AATACGGAGG  
 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700  
 48 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA  
 49 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800  
 AGTTGGTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG  
 50 TATGATTGTA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900  
 51 GAATTACTCC TTATGGAGGA A (end HD-73)

52 and equivalent nucleotide sequences coding for toxin  
 53 EW4 with the following amino acid sequence:

54 M D N N P N I N E C I P Y N C L S N P E V E V L G G E R I E  
 T G Y T P I D I S L S L T Q F L L S E F V F G A G F V L G L  
 55 V D I I W G I F G P S Q W D A F P V Q I E Q L I N Q R I E E  
 56 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
 P T N P A L R E E M R I Q F N D M N S A L T T A I P L L A V  
 57 Q N Y Q V F L L S V Y V Q A A N L H L S V L R D V S V F G Q  
 58 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
 59 L D I V A L F S N Y D S R R Y P I R T V S Q L T R E I Y T N  
 60 P V L E N F D G S F R G M A Q R I E Q N I R Q P H L M D I L  
 N S I T I Y T D V H R G F N Y W S G H Q I T A S P V G F S G  
 61 P E F A F P L F G N A G N A A P P V L V S L T G L G I F R T

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62 L S S P L Y R R I I L G S G P N N Q E L F V L D G T E F S F  
 63 A S L T T N L P S T I Y R Q R G T V D S L D V I P P Q D N S  
 64 V P P R A G F S H R L S H V T M L S Q A A G A V Y T L R A Q  
 65 R P M F S W I H R S A E F N N I I A S D S I T Q I P A V K G  
 66 N F L F N G S V I S G P G F T G G D L V R L N S S G N N I Q  
 67 N R G Y I E V P I H F P S T S T R Y R V R V R Y A S V T P I  
 68 H L N V N W G N S S I F S N T V P A T A T S L D N L Q S S D  
 69 F G Y F E S A N A F T S S L G N I V G V R N F S G T A G V I  
 70 I D R F E F I P V T A T L E A E Y N L E R A Q K A V N A L F  
 71 T S T N Q L G L K T N V T D Y H I D Q V S N L V T Y L S D E  
 72 F C L D E K R E L S E K V K H A K R L S D E R N L L Q D S N  
 73 F K D I N R Q P E R G W G G S T G I T I Q G G D D V F K E N  
 74 Y V T L S G T F D E C Y P T Y L Y Q K I D E S K L K A F T R  
 75 Y Q L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P  
 76 G T G S L W P L S A Q S P I G K C G E P N R C A P H L E W N  
 77 P D L D C S C R D G E K C A H H S H H F S L D I D V G C T D  
 78 L N E D L G V W V I F K I K T Q D G H A R L G N L E F L E E  
 79 K P L V G E A L A R V K R A E K K W R D K R E K L E W E T N  
 80 I V Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M  
 I H A A D K R V H S I R E A Y L P E L S V I P G V N A A I F  
 E E L E G R I F T A F S L Y D A R N V I K N G D F N N G L S  
 C W N V K G H V D V E E Q N N Q R S V L V V P E W E A E V S  
 Q E V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H  
 E I E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y  
 T V N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S  
 V Y E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V  
 G Y V T K E L E Y F P E T D K V W I E I G E T E G T F I V D  
 S V E L L L M E E .

23. A pesticidal composition, according to claim  
 12, wherein said gene, denoted pACB-1, encoding a  
 chimeric toxin, is as follows:

(start HD-73) ATG GATAACAATC 400  
 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500  
 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG  
 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
 CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT  
 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAAGTAAAGCA 700  
 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT  
 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800  
 CAGTGGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG  
 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
 TTGAGAGATG TTTCAGTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC

16	TATCAATAGT	CGTTATAATG	ATTTAATAAG	GCTTATTGBC	AACTATACAG	1000
17	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG	
18	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAGAAGAG	AATTAACACT	1100
19	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
20	ATCCAATTCC	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
21	GTATTAGAAA	ATTTTGATGG	TAGTTTTCSA	GGCTCGGCTC	AGGGCATAGA	
22	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
23	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
24	ATGGCTTCTC	CTGTAGGGTT	TTCGGGGCCA	GAATTCACTT	TTCCGCTATA	1400
25	TGGAAGTATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
26	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
27	AATATAGGSA	TAAATAATCA	ACAACATCT	GTTCTTGACG	GGACAGAATT	
28	TGCTTATGSA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
29	GAACGSTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
30	CCTAGGCAAG	AATTTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCBTTC	1700
31	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT (end hd-73)		
32	(start	HD-1)	CCAACGT	TTTCTTGSCA	GCATCGCAGT	1900
33	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
34	AACAAAATCT	ACTAATCTTG	GCTCTGSAAC	TTCTGTGCTT	AAAGGACCAG	2000
35	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
36	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
37	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
38	GAAGACCTAT	TAATCAGGGT	AATTTTTTCA	CAACTATGAG	TAGTGGGAGT	2200
39	AATTTACAGT	CCGGAAAGCT	TAGGACTGTA	GGTTTTACTA	CTCGGTTTAA	
40	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
41	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAAGTA	
42	ACCTTTGAGG	CAGAAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
43	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
44	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
45	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
46	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
47	ATAGACAACT	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
48	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
49	TGATGAGTGC	TATCCAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAAT	
50	TAAAGGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCSA	AGATAGTCAA	2800
51	GACTTAGAAA	TCTATTTAAT	TCGCTACAA	GCAAAACATG	AAACAGTAAA	
52	TGTGCCAGGT	ACGGGTTCCCT	TATGGCCGCT	TTCAGCCCAA	AGTCCAATCG	2900
53	GAAAGTGTGG	AGAGCCGAAT	CGATGCGGCG	CACACCTTGA	ATGGAATCCT	
54	GACTTAGATT	GTTCGTGTAG	GGATGGAGAA	AAGTGTGCCC	ATCATTCGCA	3000
55	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
56	TAGGTGTATG	GGTGTCTTTT	AGAGTTAAGA	CGCAAGATGG	GCACGCAAGA	3100
57	CTAGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAAGCGCT	
58	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
59	TGGAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
60	GCTTTATTTG	TAAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
61	TGCCATGATT	CATGCGGCAG	ATAACGTTG	TCATAGCATT	CGAGAAAGCTT	
62	ATCTGCCTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTGBAA	3400
63	GAATTAGAAG	GGCGTATTTT	CACTGCATTG	TCCCTATATG	ATGCGAGAAA	
64	TGTCATTAAA	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
65	AAGGGCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTT	GGTCCTTGTT	



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66 CTTCCGGAAT GGGAAAGCAGA AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600  
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 68 GTTGCCTAAC CATTTCATGAG ATCGAGAAC AATACAGACGA ACTGAAGTTT 3700  
 69 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGTCAATC  
 72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 73 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 74 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 75 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin  
 78 ACB-1 with the following amino acid sequence:

79 MDNPNPINECIPYNCLSNPEVEVVLGGERIE  
 80 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL  
 81 VDIIWGIFGPSQWDAFLVQIEQLINQRIEE  
 82 FARNQAISRLEGLSNLYQIYAESFREWEAD  
 83 PTNPALREEMRIQFNDMNSALTTAIPLFAV  
 84 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ  
 85 RWGFDAATINSRYNDLTRLIGNYTDYAVRW  
 86 YNTGLERVWGPSRSDWVRYNQFRRELTTLTV  
 87 LDIVALFPNYDSRRYPPIRTVSQLTREIYTN  
 88 PVLENFDDGSGFRGSAQGIERSIRSPHLM DIL  
 89 NSITIIYTD AHRGYYYWSGHQIMASPVGFSG  
 90 PEFTFPLYGTMGNAAPQQRIVAQLGQGVYR  
 91 TLSSTLYRRPFNIGINNQQQLSVLDGTEFAY  
 92 GTSSNLP S AVYRKSGTVDSLNEIPPQNNNV  
 93 PPRQEFSHRLSHVSMFRSGFSNSSSVSIIRA  
 94 PTFSSWQHRS AEFNNIIIPSSQITQIPLTKST  
 95 NLGSGT SVVKGP GFTGGDILRRTSPGQIST  
 96 LRVNITAPLSQR YRVRI RYASTTNLQFHTS  
 97 IDGRFINQGNFSATMS SSGSNLQSGSFRTVG  
 98 FTTFFNF SNGSSVFTLSAHVFNSGNEVYID  
 99 RIEFVPAEVTFEAEYDLERAQKAVNELFTS  
 100 SNQIGLKT DVT DYHIDQVSNLVECLSD EFC  
 101 LDEKQELSEKVKHAKRLSDERNLLQDPNFR  
 102 GINRQLDRGWRGST DITIQGGDDVFKENYV  
 103 TLLGTFDECYPTYLYQKIDESK LKAYTRYQ  
 104 LRGYIEDS QDLEIYLIRYN AKHETVNVPGT  
 105 GSLWFLSAQSPIGKCGEPNRCAPHLEWNP D  
 106 LDCSCR DGEKCAHHS HHFSLDIDVGC TDLN  
 107 EDLG V W V I F K I K T Q D G H A R L G N L E F L E E K P  
 108 LVGEALARVKRAEKKWRDKREKLEWETNIV  
 109 YKEAKESVDALFVNSQYDQLQADTNIA MIH  
 110 AADKR VHSIREAYLPELSVIPGVNA AIFEE

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111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
114 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
118 E L L L M E E .

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24. A pesticidal composition, according to  
claim 12, wherein said gene, denoted pSYW1, encoding  
a chimeric toxin, is as follows:

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1
2
3
4          (start HD-73)          ATG GATAACAATC 400
5 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
6 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500
7 TTCTTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
8 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
9 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAGAAT
10 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700
11 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
12 ACTAATCCAG CATTAAAGAG AGAGATGCGT ATTCATTCA ATGACATGAA 800
13 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG
14 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
15 TTGAGAGATG TTTAGTGTG TGGACAAAGG TGGGGATTTG ATGCCGCGAC
16 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000
17 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG
18 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100
19 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT
20 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200
21 GTATTAGAAA ATTTTGATGG TAGTTTTTCA GGCTCGGCTC AGGGCATAGA
22 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300
23 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAATA
24 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400
25 TGGAAGTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG
26 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500
27 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAAAT
28 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600
29 GAACGCTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA
30 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTT 1700
31 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)
32          (start HD-1)          CCAACGT TTTCTTGGCA GCATCGCAGT 1900
33 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT
34 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000
35 GATTTACAGG AGGAGATATT CTTCAAGAG CTTACCTGG CCAGATTTCA
36 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100
37 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCATACA TCAATTGACG
38 GAAGACCTAT TAATCAGGGT AATTTTTTCA CAACTATGAG TAGTGGGAGT 2200
49 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA
40 CTTTTCAAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300
41 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA

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42 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 43 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT  
 44 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500  
 45 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
 46 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600  
 47 ATAGACAACT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 48 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 49 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
 50 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 51 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 52 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 53 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 54 GACTTAGATT GTTCGTGTAG GGTGGAGAA AAGTGTGCCC ATCATTGCGA 3000  
 55 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 56 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 57 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 58 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 59 TGAATGGA AACAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 60 GCTTTATTTG TAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 61 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 62 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400  
 63 GAATTAGAAG GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 64 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 65 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT  
 66 CTTCCGGAAT GGGAAGCAGA AGTGTCAACA GAAGTTCGTG TCTGTCCGGG 3600  
 67 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 68 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
 68 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 70 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 71 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC  
 72 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 73 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 74 AAGAATTAGA ATACTTCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 75 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAAATTAC TCCTTATGGA  
 76 GGAA (end HD-1)

77 and equivalent nucleotide sequences coding for toxin  
 78 SYW1 with the following amino acid sequence:

79 M D N N F N I N E C I P Y N C L S N P E V E V L G G E R I E  
 80 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
 81 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
 82 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
 83 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
 84 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
 85 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
 86 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
 87 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
 88 P V L E N F D G S F R G S A Q G I E G S I R S P H L M D I L  
 89 N S I T I Y T D A H K G E Y Y W S G H Q I M A S P V G F S G  
 90 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R

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91 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
 92 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V  
 93 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
 94 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
 95 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
 96 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
 97 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
 98 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
 99 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
 100 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
 101 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
 102 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
 103 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
 104 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
 105 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
 106 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
 107 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
 108 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
 109 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
 110 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E  
 111 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
 112 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
 113 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
 114 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
 115 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
 116 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
 117 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
 118 E L L L M E E

1 25. A recombinant DNA transfer vector comprising  
 2 DNA having the following nucleotide sequence or  
 3 equivalent nucleotide sequences containing bases whose  
 4 translated region codes for the same amino acid sequence:

5 (start HD-73) ATG GATAACAATC 400  
 6 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
 7 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTTACACCC CAATCGATAT 500  
 8 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG  
 9 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
 10 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT  
 11 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700  
 12 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT  
 13 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCATTCA ATGACATGAA 800  
 14 CAGTGGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG  
 15 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
 16 TTGAGAGATG TTTCASTGTT TGGACAAAGG TGGGGATTTG ATGCCGCGAC  
 17 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
 18 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
 19 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACT 1100  
 20 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
 21 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200  
 22 GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA

23 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 24 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA  
 25 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400  
 26 TGGAACTATG GGAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
 27 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
 28 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
 29 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
 30 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 31 CCTAGGCAAG GATTTAGTCA TCGATTAAGC CATGTTTCAA TGTTCGTTC 1700  
 32 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 33 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900  
 34 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 35 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000  
 36 GATTTACAGG AGGAGATATT CTTCGAAGAA CTTCACCTGG CCAGATTTCA  
 37 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 38 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
 39 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200  
 40 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA  
 41 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 42 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAAGTA  
 43 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 44 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT  
 45 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500  
 46 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
 47 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600  
 48 ATAGACAAC AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 49 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 50 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
 51 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 52 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AACAGTAAA  
 53 TGTGCCAGGT ACGGGTTTCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 54 GAAAGTGTTG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 55 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000  
 56 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 57 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 58 CTAGGGAAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 59 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 60 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 61 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 62 TGCCATGATT CATGCGGCAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 63 ATCTGCCTGA GCTGTCTGTG ATTCGGGGTG TCAATGCGGC TATTTTGA 3400  
 64 GAATTAGAAG GCGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 65 TGTCATTAAG AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 66 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGTG  
 67 CTTCCGGAAT GGGAGCAGA AGTGTCACAA GAAGTTCGTG TCTGTCCGGG 3600  
 68 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 69 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
 70 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 71 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 72 ATCGAGGATA TAACGAAGCT CTTTCCGTAC CAGCTGATTA TGCCTCAGTC  
 73 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 74 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 75 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 76 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 77 GGAA (end HD-1).

26. A recombinant DNA transfer vector comprising  
DNA having the following nucleotide sequence or  
equivalent nucleotide sequences containing bases whose  
translated region codes for the same amino acid sequence:

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      (start HD-1)          ATGG ATAACAATCC GAACATCAAT
6   GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
7   TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
8   TAACGCAATT TCTTTTGAGT GAATTTGTTT CCGGTGCTGG ATTTGTGTTA 700
9   GGACTAGTTG ATATAATATG GGGAAATTTT GGTCCCTCTC AATGGGACGC
10  ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAAGAATA GAAGAATTCTG 800
11  CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
12  ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
13  ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
14  CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
15  TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
16  TTCAGTSTTT GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
17  GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
18  CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
19  TTGGGTAAGG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
20  ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGGTA TCCAATTCGA 1300
21  ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
22  TTTTGATGGT AGTTTTCTGT GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
23  GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
24  GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
25  TGTAGGGTTT TCAGGACCGA AATTCGCATT CCCTTTATTT GGGAAATGCGG
26  GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
27  AGAACATTAT CTTACCTTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
28  AAATAATCAG GAACTGTTTT TCCTTGATGG AACGGAGTTT TCTTTTGCC 1700
29  CCTAACGAC CAACTTGCC  TCCACTATAT ATAGACAAAG GGGTACAGTC
30  GATTCACAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
31  GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
32  GAGCAGTTTA CACCTTGAGA GCTCAACGT  (stop HD-1)
      (start HD-73)          CCT ATGTTCTCTT
33  GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
34  ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTTAATG GTTCTGTAAT
35  TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
36  GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
37  TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
38  GATTACCTC AACGTTAATT GGGGTAATTC ATCCATTTTT TCCAATACAG
39  TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
40  TATTTTGAAG GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
41  TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
42  TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG
43  CAGAAGBGGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300
44  AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCGAAT TTAGTTACGT
45  ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400
46  GTCAAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC
47  AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCAGGAAGTA 2500
48  CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAGAA AAATTACGTC
49  ACACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600
50  AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT

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52 ATATCGAAGA TAGTCAAGAC TTAGAATCT ATTTAATTCTG CTACAATGCA 2700  
 53 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC  
 54 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCBCGCCAC 2800  
 55 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG  
 56 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900  
 57 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC  
 57 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000  
 59 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG  
 60 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100  
 61 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA  
 62 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200  
 63 TAGCATTGCA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA  
 64 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTCAC TGCATTCTCC 3300  
 65 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT  
 66 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400  
 67 AACGTTGCGT CCTTGTGTGT CCGGAATGGG AAGCAGAAST GTCACAAGAA  
 68 GTTCGTGTCT GTCCGGGTCTG TGGCTATATC CTTCGTGTCA CAGCGTACAA 3500  
 69 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA  
 70 CAGACGAACT GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAT 3600  
 71 AACACGATAA CGTGTAAATGA TTATACTGTA AATCAGAAG AATACGGAGG  
 72 TGCCTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACCAG 3700  
 73 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA  
 74 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800  
 75 AGTTGTTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG  
 76 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900  
 77 GAATTACTCC TTATGGAGGA A (end HD-73).

1 27. A recombinant DNA transfer vector comprising  
 2 DNA having the following nucleotide sequence or  
 3 equivalent nucleotide sequences containing bases whose  
 4 translated region codes for the same amino acid  
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400  
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
 8 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500  
 9 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG  
 10 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
 11 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT  
 12 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGACTAAGCA 700  
 13 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT  
 14 ACTAATCCAG CATTAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800  
 15 CAGTGCCCTT ACAACCGCTA TTCTCTTTT TGCAGTTCAA AATTATCAAG  
 16 TTCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
 17 TTGAGAGATG TTTAGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC  
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTAGAAGAG AATTAACACT 1100  
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT

22 ATCCAATTCC AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200  
 23 GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA  
 24 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
 25 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA  
 26 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACTT TTCCGCTATA 1400  
 27 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
 28 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
 29 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
 31 GAACGGTAGA TTCGCTGAAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 32 CCTAGGCAAG AATTAGTCA TCGATTAAGC CATGTTTCAA TGTTTCGTTT 1700  
 33 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 34 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900  
 35 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 36 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTGTT AAAGGACCAG 2000  
 37 GATTTACAGG AGGAGATATT CTTCAAGAA CTTACCTGG CCAGATTTCA  
 38 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 39 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
 40 GAAGACCTAT TAATCAGGGT AATTTTTTCA CAACTATGAG TAGTGGGAGT 2200  
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA  
 42 CTTTTCAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA  
 44 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 45 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT  
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTCATC AGATGAATTT 2500  
 47 TGTCTGGATG AAAAACAAGA ATTGTCCGAG AAAGTCAAC ATGCGAAGCG  
 48 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600  
 49 ATAGACAACT AGACCGTGSC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 50 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
 52 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCSA AGATAGTCAA 2800  
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAA  
 54 TGTGCCAGGT ACGGGTTCTT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 55 GAAAGTGTGG AGAGCCGAAT CGATGCGCGC CACACCTTGA ATGGAATCCT  
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCC ATCATTCGCA 3000  
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 58 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 59 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 61 TGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 62 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 63 TGCCATGATT CATGCGGCGA ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTTGAA 3400  
 65 GAATTAGAAG GCGGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 66 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 67 AAGGGCATGT AGATGTAGAA GAACAAACA ACCAACGTTT GGTCTTGT  
 68 CTTCCGAAT GGGAAAGCAGA AGTGTACAA GAAGTTCGTG TCTGTCCGGG 3600  
 69 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 70 GTTGCCTAAC CATTATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
 71 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA



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72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 73 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TCGTCAATC  
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 78 GGAA (end HD-1).

1 28. A recombinant DNA transfer vector comprising  
 2 DNA having the following nucleotide sequence or  
 3 equivalent nucleotide sequences containing bases whose  
 4 translated region codes for the same amino acid  
 5 sequence:

6 (start HD-73) ATG GATAACAATC 400  
 7 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
 8 GAAGTATTAG GTGGAGAAAG AATAGAACT GGTACACCC CAATCGATAT 500  
 9 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGTG  
 10 GATTTGTGTT AGGACTAGT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
 11 CAATGGGACG CATTTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT  
 12 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700  
 13 ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT  
 14 ACTAATCCAG CATTAGAGAG AGAGATGCGT ATTCATTCA ATGACATGAA 800  
 15 CAGTGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG  
 16 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
 17 TTGAGAGATG TTTCASTGT TGGACAAAGG TGGGGATTTG ATGCCGCGAC  
 18 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
 19 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
 20 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTAGAAGAG AATTAACT 1100  
 21 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
 22 ATCCAATTCG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200  
 23 GTATTAGAAA ATTTTGATGG TAGTTTTGGA GGCTCGGCTC AGGGCATAGA  
 24 AGGAAGTATT AGGAGTCCAC ATTTGATGGA TACTTTAAC AGTATAACCA 1300  
 25 TCTATACGGA TGCTCATAAA GGGGAATATT ATTGGTCAGG GCATCAAATA  
 26 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCATT TTCCGCTATA 1400  
 27 TGGAACTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
 28 GTCAGGGCGT GTATAGAACA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
 29 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
 30 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
 31 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
 32 CCTAGGCAAG GATTTAGTCA TCGATTAGC CATGTTTCAA TGTTTCGTTT 1700  
 33 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
 34 (start HD-1) CCAACGT TTTCTTGGCA GCATCGCAGT 1900  
 35 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
 36 AACAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000  
 37 GATTTACAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTC  
 38 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
 39 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCATACA TCAATTGACG

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40 GAAGACCTAT TAATCAGGGT AATTTTTCAG CAACTATGAG TAGTGGGAGT 2200  
 41 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA  
 42 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
 43 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA  
 44 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
 45 GCTGTTTACT TCTTCCAATC AAATCGGGTT AAAACAGAT GTGACGGATT  
 46 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500  
 47 TGTCTGAGTG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
 48 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAAACTTC AGAGGGATCA 2600  
 49 ATAGACAACCT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
 50 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 51 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
 52 TAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 53 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 54 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 55 GAAAGTGTGG AGAGCCGAAT CGATGCGCSC CACACCTTGA ATGGAATCCT  
 56 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000  
 57 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 58 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 59 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 60 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 61 TGGAAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 62 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 63 TGCCATGATT CATGCGGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 64 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTGA 3400  
 65 GAATTAGAA GGCATATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
 66 TGTCATTAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAACGTGA 3500  
 67 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT  
 68 CTTCCGGAAT GGGAAAGCAGA AGTGTACAAA GAAGTTCTGT TCTGTCCGGG 3600  
 69 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 70 GTTGCCTAAC CATTCATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
 71 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 72 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 73 ATCGAGGATA TAACGAAGCT CTTCCGTAC CAGCTGATTA TCGTCACTC  
 74 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 75 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 76 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 77 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 78 GGAA (end HD-1).

1 29. The DNA transfer vector of claim 25 trans-  
 2 ferred to and replicated in a prokaryotic or lower  
 3 eukaryotic microorganism.

1           30. The DNA transfer vector of claim 26 trans-  
2           ferred to and replicated in a prokaryotic or lower  
3           eukaryotic microorganism.

1           31. The DNA transfer vector of claim 27 trans-  
2           ferred to and replicated in a prokaryotic or lower  
3           eukaryotic microorganism.

1           32. The DNA transfer vector of claim 28 trans-  
2           ferred to and replicated in a prokaryotic or lower  
3           eukaryotic microorganism.

1           33. Plasmid pEW1 as shown in FIGURE 1 of the  
2           drawings.

1           34. Plasmid pEW2 as shown in FIGURE 2 of the  
2           drawings.

1           35. Plasmid pEW3 as shown in FIGURE 3 of the  
2           drawings.

1           36. Plasmid pEW4 as shown in FIGURE 4 of the  
2           drawings.

1           37. Plasmid pACB-1, having the construction of  
2           plasmid pEW3 except that the DNA encoding aspartic  
3           acid at position 411 is converted to encode asparagine,  
4           and the DNA encoding glycine at position 425 is con-  
5           verted to encode glutamic acid.

1           38. Plasmid pSYW1, having the construction of plasmid  
2           pEW3 except that the DNA encoding arginine at position  
3           289 is converted to encode glycine, the DNA encoding  
4           arginine at position 311 is converted to encode lysine,  
5           and the DNA encoding tyrosine at position 313 is conver-  
6           ted to encode glutamate.

1 39. A microorganism transformed by the transfer  
2 vector of claim 25.

1 40. A microorganism transformed by the transfer  
2 vector of claim 26.

1 41. A microorganism transformed by the transfer  
2 vector of claim 27.

1 42. A microorganism transformed by the transfer  
2 vector of claim 28.

1 43. E. coli (pEW3), a microorganism according  
2 to claim 39.

1 44. E. coli (pEW4), a microorganism according to  
2 claim 40.

1 45. E. coli (pACB-1), a microorganism according  
2 to claim 41.

1 46. E. coli (pSYW1), a microorganism according  
2 to claim 42.

1 47. A process for preparing pesticidal chimeric  
2 toxin EW3 having the following amino acid sequence:

3 MDNNPNINEDCIPYNCLSNP E V E V L G G E R I E  
4 T G Y T P I D I S L S L T Q F L L S E F V P G A G F V L G L  
5 V D I I W G I F G P S Q W D A F L V Q I E Q L I N Q R I E E  
6 F A R N Q A I S R L E G L S N L Y Q I Y A E S F R E W E A D  
7 P T N P A L R E E M R I Q F N D M N S A L T T A I P L F A V  
8 Q N Y Q V P L L S V Y V Q A A N L H L S V L R D V S V F G Q  
9 R W G F D A A T I N S R Y N D L T R L I G N Y T D Y A V R W  
10 Y N T G L E R V W G P D S R D W V R Y N Q F R R E L T L T V  
11 L D I V A L F P N Y D S R R Y P I R T V S Q L T R E I Y T N  
12 P V L E N F D G S F R G S A Q G I E R S I R S P H L M D I L  
13 N S I T I Y T D A H R G Y Y Y W S G H Q I M A S P V G F S G

14 P E F T F P L Y G T M G N A A P Q Q R I V A Q L G Q G V Y R  
15 T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y  
16 G T S S N L P S A V Y R K S G T V D S L D E I P P Q N N N V  
17 P P R Q G F S H R L S H V S M F R S G F S N S S V S I I R A  
18 P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T  
19 N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T  
20 L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S  
21 I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G  
22 F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D  
23 R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S  
24 S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C  
25 L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R  
26 G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V  
27 T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q  
28 L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T  
29 G S L W P L S A Q S P I G K C G E F N R C A P H L E W N P D  
30 L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N  
31 E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P  
32 L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V  
33 Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H  
34 A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E  
35 L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W  
36 N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E  
37 V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I  
38 E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V  
39 N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y  
40 E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y  
41 V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V  
42 E L L L M E E

43 which comprises culturing a prokaryotic microbe  
44 hosting a recombinant DNA transfer vector, denoted  
45 pEW3, comprising DNA having the following nucleotide  
46 sequence or equivalent nucleotide sequences containing  
47 bases whose translated region codes for the same  
48 amino acid sequence:

49 (start HD-73) ATG GATAACAATC 400  
50 CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA  
51 GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500  
52 TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG  
53 GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600  
54 CAATGGGACG CATTCTTGTT ACAAAATTGAA CAGTTAATTA ACCAAAGAAT  
55 AGAAGAATTC GCTAGGAACC AAGCCATTTT TAGATTAGAA GGAATAAGCA 700  
56 ATCTTTATCA AATTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT  
57 ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCATTCA ATGACATGAA 800  
58 CAGTGGCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG  
59 TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900  
60 TTGAGAGATG TTTAGTGTT TGGACAAAGG TGGGGATTG ATGCCGCGAC

61 TATCAATAGT CGTTATAATG ATTTAACTAG GCTTATTGGC AACTATACAG 1000  
62 ATTATGCTGT ACGCTGGTAC AATACGGGAT TAGAACGTGT ATGGGGACCG  
63 GATTCTAGAG ATTGGGTAAG GTATAATCAA TTTAGAAGAG AATTAACACT 1100  
64 AACTGTATTA GATATCGTTG CTCTGTTCCC GAATTATGAT AGTAGAAGAT  
65 ATCCAATTGG AACAGTTTCC CAATTAACAA GAGAAATTTA TACAAACCCA 1200  
66 GTATTAGAAA ATTTTGATGG TAGTTTTCSA GGCTCGGCTC AGGGCATAGA  
67 AAGAAGTATT AGGAGTCCAC ATTTGATGGA TATACTTAAC AGTATAACCA 1300  
68 TCTATACGGA TGCTCATAGG GGTATTATT ATTGGTCAGG GCATCAAATA  
69 ATGGCTTCTC CTGTAGGGTT TTCGGGGCCA GAATTCACCT TTCCGCTATA 1400  
70 TGGAAGTATG GGAAATGCAG CTCCACAACA ACGTATTGTT GCTCAACTAG  
71 GTCAGGGCGT GATAGAACAA TTATCGTCCA CTTTATATAG AAGACCTTTT 1500  
72 AATATAGGGA TAAATAATCA ACAACTATCT GTTCTTGACG GGACAGAATT  
73 TGCTTATGGA ACCTCCTCAA ATTTGCCATC CGCTGTATAC AGAAAAAGCG 1600  
74 GAACGGTAGA TTCGCTGGAT GAAATACCGC CACAGAATAA CAACGTGCCA  
75 CCTAGGCAAG GATTTAGTCA TCGATTAAAG CATGTTTCAA TGTTCGTTT 1700  
76 AGGCTTTAGT AATAGTAGTG TAAGTATAAT AAGAGCT (end hd-73)  
77 (start HD-1) CCAACGT TTTCTTGCCA GCATCGCAGT 1900  
78 GCTGAATTTA ATAATATAAT TCCTTCATCA CAAATTACAC AAATACCTTT  
79 AACAAAATCT ACTAATCTTG GCTCTGGAAC TTCTGTCGTT AAAGGACCAG 2000  
80 GATTTCAGG AGGAGATATT CTTGGAAGAA CTTACCTGG CCAGATTTC  
81 ACCTTAAGAG TAAATATTAC TGCACCATTA TCACAAAGAT ATCGGGTAAG 2100  
82 AATTCGCTAC GCTTCTACTA CAAATTTACA ATTCCATACA TCAATTGACG  
83 GAAGACCTAT TAATCAGGGT AATTTTTTCA CAACTATGAG TAGTGGGAGT 2200  
84 AATTTACAGT CCGGAAGCTT TAGGACTGTA GGTTTTACTA CTCCGTTTAA  
85 CTTTTCAAAT GGATCAAGTG TATTTACGTT AAGTGCTCAT GTCTTCAATT 2300  
86 CAGGCAATGA AGTTTATATA GATCGAATTG AATTTGTTCC GGCAGAAGTA  
87 ACCTTTGAGG CAGAATATGA TTTAGAAAGA GCACAAAAGG CGGTGAATGA 2400  
88 GCTGTTTACT TCTTCCAATC AAATCGGGT AAAACAGAT GTGACGGATT  
89 ATCATATTGA TCAAGTATCC AATTTAGTTG AGTGTTTATC AGATGAATTT 2500  
90 TGTCTGGATG AAAACAAGA ATTGTCCGAG AAAGTCAAAC ATGCGAAGCG  
91 ACTTAGTGAT GAGCGGAATT TACTTCAAGA TCCAACTTC AGAGGGATCA 2600  
92 ATAGACAACCT AGACCGTGGC TGGAGAGGAA GTACGGATAT TACCATCCAA  
93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
95 TAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCSA AGATAGTCAA 2800  
96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
97 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
98 GAAAGTGTGG AGAGCCGAAT CGATGCGGCG CACACCTTGA ATGGAATCCT  
99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000  
100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
102 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
103 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
104 TGGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
106 TGCCATGATT CATGCGGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
107 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGGC TATTTTTGAA 3400  
108 GAATTAGAAG GCGGTATTTT CACTGCATTC TCCCTATATG ATGCGAGAAA  
109 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGACGTGA 3500  
110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTT GGTCTTGT  
111 CTTCCGGAAT GGGAGGAGAG AGTGTACAAA GAAGTTCGTG TCTGTCCGGG 3600  
112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
113 GTTGCATAAC CATTCATGAG ATCGAGACA ATACAGACGA ACTGAAGTTT 3700  
114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA

M12C1FDF3D2

115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC  
 117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 120 GAAACGGAAG GAACATTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 121 GGAA (end HD-1).

1 48. A process for preparing pesticidal chimeric  
 2 toxin EW4 having the following amino acid sequence:

3 MDNNPNIN ECIFYNCLSNPEVEVLGGERIE  
 4 TGYTPIDISLSLTQFLLSEFVPGAGFVLGL  
 5 VDI IWGIFGPSQWDAFPVQIEQLINQRIEE  
 6 FARNQAI SRLEGLSNLYQIYAESFREWEAD  
 7 PTNPALREEMRIQFNDMNSALTTAIPLLAV  
 8 QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ  
 9 RWGFDAATINSRYNDLTRRLIGNYTDYAVRW  
 10 YNTGLERVWGPDSRDWVRYNQFRRELTTLTV  
 11 LDIVALFSNYDSRRYP IRTVSQLTREIYTN  
 12 PVLENFDFGSFRGM AQRIEQNIRQPHLMDIL  
 13 NSIT IYTDVHRGFNYWSGHQITASPVGFSG  
 14 PEFAPFLFGNAGNAAPPVLVSLTGLGIFRT  
 15 LSSPLYRRIILGSGFPNNQELFVL DGT EFSF  
 16 ASLTTNLPSTIYRQRGTVDSDL DVI PPQ DNS  
 17 VPPRAGF SHRLSHVTMLSQAAGAVYTLRAQ  
 18 RPFMFSWIHRSAEFNNIIASDSITQIPAVKG  
 19 NFLFN GSVISGPGFTGGDLVRLNSSSGNNIQ  
 20 NRGYIEVP IHF PSTSTRYRVRYASVTFPI  
 21 HLN VNWGNSSIFSNTVPATATSLDNLQSSD  
 22 FGYFESANAF TSSSLGNIVGV RNFSGTAGVI  
 23 IDRFEFIPVTATLEAEYNLERAQKAVNALF  
 24 TSTNOLGLKTNVTDYHIDQVSNLV TYLSDE  
 25 FCLDEKRELSEKVKHAKRLSDERNLLQDSN  
 26 FKDINRQPERGWWGGSTGITIQGGDDVFKEN  
 27 YVTLSGTFDECYPTYLYQKIDESK LKAFTR  
 28 YQLRGYIEDSQDLEIYLI RYNAKHETVNVP  
 29 GTGSLWFLSAQSPIGKCGEPNRCAPHLEWN  
 30 PDLDCSCRDGEEKCAHHSHHFSLDIDV GCTD  
 31 LNEDLGVWVIFKIKTQDGHARLGNLEFLEE  
 32 KPLVGEALARVKRAEKKWRDKREKLEWETN  
 33 IVYKEAKESVDALFVNSQYDQLQADTNIAM  
 34 IHAADKRVHSIREAYLPELSVIPGVNAAIF  
 35 EELEGRIFTAFSELYDARNVIKNGDFNGLS  
 36 CWNVKGHV DVEEQNNQRSVLV VPEWEAEVS  
 37 QEV RVC PGRGVI LRVTAYKEGYGEGCVTIH  
 38 EIENNTDELKFSN CVEEEIYPNNTVTCNDY  
 39 TVNQEEYGGAYTSRNRGYNEAPSVPADYAS  
 40 VYEEKSYTDGRRENPCFNRGYRDYTPLPV  
 41 GYVTKELEYFPETDKVWIEIGETEGTFIVD  
 42 SVELLLMEE

10035050 122701

43 which comprises culturing a prokaryotic microbe  
44 hosting a recombinant DNA transfer vector, denoted  
45 pEW4, comprising DNA having the following nucleotide  
46 sequence or equivalent nucleotide sequences containing  
47 bases whose translated region codes for the same amino  
48 acid sequence:

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49          (start HD-1)          ATGG ATAACAATCC GAACATCAAT
50 GAATGCATTC CTTATAATTG TTTAAGTAAC CCTGAAGTAG AAGTATTAGG 600
51 TGGAGAAAGA ATAGAAACTG GTTACACCCC AATCGATATT TCCTTGTCGC
52 TAACGCAATT TCTTTTGAGT GAATTTGTTC CCGGTGCTGG ATTTGTGTTA 700
53 GGACTAGTTG ATATAATATG GGGGAATTTT GGTCCCTCTC AATGGGACGC
54 ATTTCTGTGA CAAATTGAAC AGTTAATTAA CCAAGAATAA GAAGAATTCTG 800
55 CTAGGAACCA AGCCATTTCT AGATTAGAAG GACTAAGCAA TCTTTATCAA
56 ATTTACGCAG AATCTTTTAG AGAGTGGGAA GCAGATCCTA CTAATCCAGC 900
57 ATTAAGAGAA GAGATGCGTA TTCAATTCAA TGACATGAAC AGTGCCCTTA
58 CAACCGCTAT TCCTCTTTTG GCAGTTCAAA ATTATCAAGT TCCTCTTTTA 1000
59 TCAGTATATG TTCAAGCTGC AAATTTACAT TTATCAGTTT TGAGAGATGT
60 TTCAGTGTTT GGACAAAGGT GGGGATTTGA TGCCGCGACT ATCAATAGTC 1100
61 GTTATAATGA TTTAACTAGG CTTATTGGCA ACTATACAGA TTATGCTGTG
62 CGCTGGTACA ATACGGGATT AGAGCGTGTA TGGGGACCGG ATTCTAGAGA 1200
63 TTGGGTAAAG TATAATCAAT TTAGAAGAGA GCTAACACTT ACTGTATTAG
64 ATATCGTTGC TCTATTCTCA AATTATGATA GTCGAAGSTA TCCAATTCSA 1300
65 ACAGTTTCCC AATTAACAAG AGAAATTTAT ACGAACCCAG TATTAGAAAA
66 TTTTGATGGT AGTTTTCGTG GAATGGCTCA GAGAATAGAA CAGAATATTA 1400
67 GGCAACCACA TCTTATGGAT ATCCTTAATA GTATAACCAT TTATACTGAT
68 GTGCATAGAG GCTTTAATTA TTGGTCAGGG CATCAAATAA CAGCTTCTCC 1500
69 TGTAGGGTTT TCAGGACCAG AATTCGCATT CCCTTTATTT GGGGAATGCGG
70 GGAATGCAGC TCCACCCGTA CTTGTCTCAT TAACTGGTTT GGGGATTTTT 1600
71 AGAACATTAT CTTACCTTT ATATAGAAGA ATTATACTTG GTTCAGGCCC
72 AAATAATCAG GAACTGTTTG TCCTTGATGG AACGGAGTTT TCTTTTGCCT 1700
73 CCCTAACGAC CAACTTGCTT TCCACTATAT ATAGACAAAG GGGTACAGTC
74 GATTCACTAG ATGTAATACC GCCACAGGAT AATAGTGTAC CACCTCGTGC 1800
75 GGGATTTAGC CATCGATTGA GTCATGTTAC AATGCTGAGC CAAGCAGCTG
76 GAGCAGTTTA CACCTTGAGA GCTCAACGT (stop HD-1)
77          (start HD-73)          CCT ATGTTCTCTT
78 GGATACATCG TAGTGCTGAA TTTAATAATA TAATTGCATC GGATAGTATT 1800
79 ACTCAAATCC CTGCAGTGAA GGGAAACTTT CTTTTAATG GTTCTGTAAT
80 TTCAGGACCA GGATTTACTG GTGGGGACTT AGTTAGATTA AATAGTAGTG 1900
81 GAAATAACAT TCAGAATAGA GGGTATATTG AAGTTCCAAT TCACTTCCCA
82 TCGACATCTA CCAGATATCG AGTTCGTGTA CGGTATGCTT CTGTAACCCC 2000
83 GATTACCTC AACGTTAATT GGGGTAATTC ATCCATTTTT TCCAATACAG
84 TACCAGCTAC AGCTACGTCA TTAGATAATC TACAATCAAG TGATTTTGGT 2100
85 TATTTTGAAG GTGCCAATGC TTTTACATCT TCATTAGGTA ATATAGTAGG
86 TGTTAGAAAT TTTAGTGGGA CTGCAGGAGT GATAATAGAC AGATTTGAAT 2200
87 TTATTCCAGT TACTGCAACA CTCGAGGCTG AATATAATCT GGAAAGAGCG

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88 CAGAAGGCGG TGAATGCGCT GTTTACGTCT ACAAACCAAC TAGGGCTAAA 2300  
 89 AACAAATGTA ACGGATTATC ATATTGATCA AGTGTCCAAT TTAGTTACGT  
 90 ATTTATCGGA TGAATTTTGT CTGGATGAAA AGCGAGAATT GTCCGAGAAA 2400  
 91 GTCAACATG CGAAGCGACT CAGTGATGAA CGCAATTTAC TCCAAGATTC  
 92 AAATTTCAAA GACATTAATA GGCAACCAGA ACGTGGGTGG GGCGBAAGTA 2500  
 93 CAGGGATTAC CATCCAAGGA GGGGATGACG TATTTAAGA AAATTACGTC  
 94 ACACTATCAG GTACCTTTGA TGAGTGCTAT CCAACATATT TGTATCAAAA 2600  
 95 AATCGATGAA TCAAAATTAA AAGCCTTTAC CCGTTATCAA TTAAGAGGGT  
 96 ATATCGAAGA TAGTCAAGAC TTAGAAATCT ATTTAATTCT CTACAATGCA 2700  
 97 AAACATGAAA CAGTAAATGT GCCAGGTACG GGTTCCTTAT GGCCGCTTTC  
 98 AGCCCAAAGT CCAATCGGAA AGTGTGGAGA GCCGAATCGA TGCAGGCCAC 2800  
 99 ACCTTGAATG GAATCCTGAC TTAGATTGTT CGTGTAGGGA TGGAGAAAAG  
 100 TGTGCCCATC ATTCGCATCA TTTCTCCTTA GACATTGATG TAGGATGTAC 2900  
 101 AGACTTAAAT GAGGACCTAG GTGTATGGGT GATCTTTAAG ATTAAGACGC  
 102 AAGATGGGCA CGCAAGACTA GGGAACTAG AGTTTCTCGA AGAGAAACCA 3000  
 103 TTAGTAGGAG AAGCGCTAGC TCGTGTGAAA AGAGCGGAGA AAAAATGGAG  
 104 AGACAAACGT GAAAAATTGG AATGGGAAAC AAATATCGTT TATAAGAGG 3100  
 105 CAAAAGAATC TGTAGATGCT TTATTTGTAA ACTCTCAATA TGATCAATTA  
 106 CAAGCGGATA CGAATATTGC CATGATTCAT GCGGCAGATA AACGTGTTCA 3200  
 107 TAGCATTCTGA GAAGCTTATC TGCCTGAGCT GTCTGTGATT CCGGGTGTCA  
 108 ATGCGGCTAT TTTTGAAGAA TTAGAAGGGC GTATTTTTCAC TGCATTCTCC 3300  
 109 CTATATGATG CGAGAAATGT CATTAAAAAT GGTGATTTTA ATAATGGCTT  
 110 ATCCTGCTGG AACGTGAAAG GGCATGTAGA TGTAGAAGAA CAAAACAACC 3400  
 111 AACGTTCGGT CCTTGTGTTT CCGGAATGGG AAGCAGAAGT GTCACAAGAA  
 112 GTTCGTGTCT GTCCGGGTCT TGGCTATATC CTTCTGTGTA CAGCGTACAA 3500  
 113 GGAGGGATAT GGAGAAGGTT GCGTAACCAT TCATGAGATC GAGAACAATA  
 114 CAGACGAACG GAAGTTTAGC AACTGCGTAG AAGAGGAAAT CTATCCAAAT 3600  
 115 AACACGGTAA CGTGAATGA TTATACTGTA AATCAAGAAG AATACGGAGG  
 116 TGCGTACACT TCTCGTAATC GAGGATATAA CGAAGCTCCT TCCGTACAG 3700  
 117 CTGATTATGC GTCAGTCTAT GAAGAAAAAT CGTATACAGA TGGACGAAGA  
 118 GAGAATCCTT GTGAATTTAA CAGAGGGTAT AGGGATTACA CGCCACTACC 3800  
 119 AGTTGSTTAT GTGACAAAAG AATTAGAATA CTTCCAGAA ACCGATAAGG  
 120 TATGGATTGA GATTGGAGAA ACGGAAGGAA CATTTATCGT GGACAGCGTG 3900  
 121 GAATTACTCC TTATGGAGGA A (end HD-73).

49. A process for preparing pesticidal chimeric  
 toxin ACB-1 having the following amino acid sequence:

MDN.NPN INECIPYNC LSNFEVEVLGGERIE  
 TGYTPIDISLSLTQFL LSEFVFGAGFVLGL  
 VDI IWGIFGPSQWDAFLVQIEQLINQRIEE  
 FARNQAISRLEGLSNLYQIYAESFREWEAD  
 PTNPALREEMRIQFNDMNSALTTAIFLFAV  
 QNYQVPLLSVYVQAANLHLSVLRDVS VFGQ  
 RWGFDAATINSRYNDLTR LIGNYTDYAVRW  
 YN.TGLERVWGPDSRDWVRYNQFRRELT LTV  
 LDIVALFPNYDSRRYP IRTVSQLTREIYTN  
 PVLENFDGSGFRGSAQGIERSIRSPHLM DIL  
 NSITIYTDAHRGY YWSGHQIMASPVGFSG  
 PEFTFPLY.GTMGNAAPQQRIVAQ LGGGVYR

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15  T L S S T L Y R R P F N I G I N N Q Q L S V L D G T E F A Y
16  G T S S N L P S A V Y R K S G T V D S L N E I P P Q N N N V
17  P P R Q E F S H R L S H V S M F R S G F S N S S V S I I R A
18  P T F S W Q H R S A E F N N I I P S S Q I T Q I P L T K S T
19  N L G S G T S V V K G P G F T G G D I L R R T S P G Q I S T
20  L R V N I T A P L S Q R Y R V R I R Y A S T T N L Q F H T S
21  I D G R P I N Q G N F S A T M S S G S N L Q S G S F R T V G
22  F T T P F N F S N G S S V F T L S A H V F N S G N E V Y I D
23  R I E F V P A E V T F E A E Y D L E R A Q K A V N E L F T S
24  S N Q I G L K T D V T D Y H I D Q V S N L V E C L S D E F C
25  L D E K Q E L S E K V K H A K R L S D E R N L L Q D P N F R
26  G I N R Q L D R G W R G S T D I T I Q G G D D V F K E N Y V
27  T L L G T F D E C Y P T Y L Y Q K I D E S K L K A Y T R Y Q
28  L R G Y I E D S Q D L E I Y L I R Y N A K H E T V N V P G T
29  G S L W P L S A Q S P I G K C G E P N R C A P H L E W N P D
30  L D C S C R D G E K C A H H S H H F S L D I D V G C T D L N
31  E D L G V W V I F K I K T Q D G H A R L G N L E F L E E K P
32  L V G E A L A R V K R A E K K W R D K R E K L E W E T N I V
33  Y K E A K E S V D A L F V N S Q Y D Q L Q A D T N I A M I H
34  A A D K R V H S I R E A Y L P E L S V I P G V N A A I F E E
35  L E G R I F T A F S L Y D A R N V I K N G D F N N G L S C W
36  N V K G H V D V E E Q N N Q R S V L V L P E W E A E V S Q E
37  V R V C P G R G Y I L R V T A Y K E G Y G E G C V T I H E I
38  E N N T D E L K F S N C V E E E I Y P N N T V T C N D Y T V
39  N Q E E Y G G A Y T S R N R G Y N E A P S V P A D Y A S V Y
40  E E K S Y T D G R R E N P C E F N R G Y R D Y T P L P V G Y
41  V T K E L E Y F P E T D K V W I E I G E T E G T F I V D S V
42  E L L L M E E

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43 which comprises culturing a prokaryotic microbe  
44 hosting a recombinant DNA transfer vector, denoted  
45 pACB-1, comprising DNA having the following nucleotide  
46 sequence or equivalent nucleotide sequences containing  
47 bases whose translated region codes for the same  
48 amino acid sequence:

```

49          (start HD-73)          ATG GATAACAATC 400
50  CGAACATCAA TGAATGCATT CCTTATAATT GTTTAAGTAA CCCTGAAGTA
51  GAAGTATTAG GTGGAGAAAG AATAGAAACT GGTACACCC CAATCGATAT 500
52  TTCCTTGTCG CTAACGCAAT TTCTTTTGAG TGAATTTGTT CCCGGTGCTG
53  GATTTGTGTT AGGACTAGTT GATATAATAT GGGGAATTTT TGGTCCCTCT 600
54  CAATGGGACG CATTCTTGT ACAAATTGAA CAGTTAATTA ACCAAAGAAT
55  AGAAGAATTC GCTAGGAACC AAGCCATTC TAGATTAGAA GGACTAAGCA 700
56  ATCTTTATCA AATTTACGCA GAATCTTTTA GAGAGTGGGA AGCAGATCCT
57  ACTAATCCAG CATTAAAGAGA AGAGATGCGT ATTCAATTCA ATGACATGAA 800
58  CAGTGCCCTT ACAACCGCTA TTCCTCTTTT TGCAGTTCAA AATTATCAAG
59  TTCCTCTTTT ATCAGTATAT GTTCAAGCTG CAAATTTACA TTTATCAGTT 900
60  TTGAGAGATG TTTCAAGTGT TGGACAAAGG TGGGGATTG ATGCCGCGAC

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61	TATCAATAGT	CGTTATAATG	ATTAACTAG	GCTTATTGBC	AACATATACG	1000
62	ATTATAGTGT	ACGCTGGTAC	AATACGGGAT	TAGAACGTGT	ATGGGGACCG	
63	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	TTTAGAAGAG	AATTAACACT	1100
64	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
65	ATCCAATTCC	AACAGTTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
66	GTATTAGAAA	ATTTTGATGG	TAGTTTTCSA	GGCTCGGCTC	AGGGCATAGA	
67	AAGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
68	TCTATACGGA	TGCTCATAGG	GGTTATTATT	ATTGGTCAGG	GCATCAAATA	
69	ATGGCTTCTC	CTGTAGGGTT	TTGGGGGCCA	GAATTCACCT	TTCCGCTATA	1400
70	TGGAAGTATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
71	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
72	AATATAGGGA	TAAATAATCA	ACAACATATC	GTTCTTGACG	GGACAGAATT	
73	TGCTTATGGA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
74	GAACGGTAGA	TTCGCTGAAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
75	CCTAGGCAAG	AATTTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCGTTT	1700
76	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT (end hd-73)		
77	(start	HD-1)	CCAACGT	TTTCTTGSCA	GCATCGCAGT	1900
78	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
79	AACAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTGCTT	AAAGGACCAG	2000
80	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
81	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
82	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
83	GAAGACCTAT	TAATCAGGGT	AATTTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
84	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTTA	
85	CTTTTCAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
86	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAGTA	
87	ACCTTTGAGG	CAGAATATGA	TTTAGAAAGA	GCACAAAAGG	CGGTGAATGA	2400
88	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAAAACAGAT	GTGACGGATT	
89	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
90	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
91	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGG	TCCAAACTTC	AGAGGGATCA	2600
92	ATAGACAAC	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
93	GGAGGCGATG	ACGTATTCAA	AGAGAATTAC	GTTACGCTAT	TGGGTACCTT	2700
94	TGATGAGTGC	TATCCAACGT	ATTTATATCA	AAAAATAGAT	GAGTCGAAT	
95	TAAAGGCCTA	TACCCGTTAT	CAATTAAGAG	GGTATATCSA	AGATAGTCAA	2800
96	GACTTAGAAA	TCTATTTAAT	TCGCTACAA	GCAAAACATG	AAACAGTAAA	
97	TGTGCCAGGT	ACGGGTTCC	TATGGCCGCT	TTGAGCCCAA	AGTCCAATCG	2900
98	GAAAGTGTGG	AGAGCCGAAT	CGATGCGCGC	CACACCTTGA	ATGGAATCCT	
99	GACTTAGATT	GTTCTGTAG	GGATGGAGAA	AAGTGTGCC	ATCATTCGCA	3000
100	TCATTTCTCC	TTAGACATTG	ATGTAGGATG	TACAGACTTA	AATGAGGACC	
101	TAGGTGATG	GGTGATCTTT	AAGATTAGGA	CGCAAGATGG	GCACGCAAGA	3100
102	CTAGGGAATC	TAGAGTTTCT	CGAAGAGAAA	CCATTAGTAG	GAGAAAGCGCT	
103	AGCTCGTGTG	AAAAGAGCGG	AGAAAAAATG	GAGAGACAAA	CGTGAAAAAT	3200
104	TGGAATGGGA	AACAAATATC	GTTTATAAAG	AGGCAAAAGA	ATCTGTAGAT	
105	GCTTTATTTG	TAAACTCTCA	ATATGATCAA	TTACAAGCGG	ATACGAATAT	3300
106	TGCCATGATT	CATGCGGCAG	ATAAACGTGT	TCATAGCATT	CGAGAAGCTT	
107	ATCTGCTTGA	GCTGTCTGTG	ATTCCGGGTG	TCAATGCGGC	TATTTTTGAA	3400
108	GAATTAGAAG	GGCGTATTTT	CACTGCATTC	TCCCTATATG	ATGCGAGAAA	
109	TGTCATTAAA	AATGGTGATT	TTAATAATGG	CTTATCCTGC	TGGAACGTGA	3500
110	AAGGGCATGT	AGATGTAGAA	GAACAAAACA	ACCAACGTTT	GGTCTTGT	
111	CTTCCGGAAT	GGGAAGCAGA	AGTGTACAAA	GAAGTTCGTG	TCTGTCCGGG	3600
112	TCGTGGCTAT	ATCCTTCGTG	TCACAGCGTA	CAAGGAGGGA	TATGGAGAAG	

113 GTTGCCTAAC CATTCATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
 114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC  
 117 TATGAAGAAA AATCGTATAC ASATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 120 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 121 GGAA (end HD-1) .

1 50. A process for preparing pesticidal chimeric  
 2 toxin SYW1 having the following amino acid sequence:

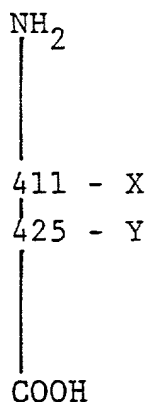
3 MDNNPNIN ECIPYNCLSNPEVEVLGGERIE  
 4 TGYTFIDISLSLTQFLLSEFVPGAGFVLGL  
 5 VDIIWGIFGFSQWDAFLVQIEQLINQRIEE  
 6 FARNQAISRLEGLSNLYQIYAESFREWEAD  
 7 PTNFPALREEMRIQFNDMNSALTTAIPLFAV  
 8 QNYQVPLLSVYVQAANLHLSVLRDVSVFGQ  
 9 RWGFDAAATINSRYNDLTRLIGNYT DYAVRW  
 10 YNTGLERVWGPDSRDWVRYNQFRRELT LT V  
 11 LDIVALFPNYDSRRYP IRTVSQLTREIYT N  
 12 PVLENFDGSGFRGSAQGGIEGSI RSPHLM DIL  
 13 NSIT IYTD AHKG EY YWSGHQIMASPVGFSG  
 14 PEFTFPLYGTMGNAAPQQRI VAQLGGGVYR  
 15 TSSSTLYRRPFNIGINNQQLSVLDGTEFAY  
 16 GTSSNLP S AVYRKSGTVDSLDEIPPQNNNV  
 17 PPRQGFSHRLSHVSMFRSGFSNS SVS IIRA  
 18 PTF SWQHRS AEFNNIIPSSQITQIPLTKST  
 19 NLGSGT SVVKGP GFTGGDILRRTSPGQIST  
 20 LRVNITAPLSQRYRVRIRYASTTNLQFHTS  
 21 IDGRPINQGNFSATMSSG SNLQSGSFRTVG  
 22 FTT P FNFSNGSSVFTLSAHVFNSGNEVYID  
 23 RIEFVPAEVTFEAEYDLERAQKAVNELFTS  
 24 SNQIGLKT DVT DYHIDQVSNLVECLSD EFC  
 25 LDEKQELSEKVKHAKRLSDERNLLQDPNFR  
 26 GINRQLDRGW RGST DITIGGGDDVFKENYV  
 27 TLLGT FDECYPT YLYQK IDESKLKAYTRYQ  
 28 LRGYIEDSQDLEIYLIRYN AKHETVNVPGT  
 29 GSLWPLSAQSPIGKCGEPNRCAPHLEWNP D  
 30 LDCSCR DGEKCAHHS HHFSLDIDVGCTDLN  
 31 EDLGVWVIFKIKTQDGHARLGNLEFLEEK P  
 32 LVGEALARVKRAEKKWRDKREKLEWETNI V  
 33 YKEAKESVDALFVNSQYDQLQADTNIA MIH  
 34 AADKRVHSIREAYLPELSVIPGVNA AIFEE  
 35 LEGRIFTA FSLYDARNV IKN GDFNGLSCW  
 36 NVKGHV DVEEQNNQRNSVLVLP EWAEVSE  
 37 VRVCPGRGYILRV TAYKEGYGEGCVTIHEI  
 38 ENNTDELKFSNCVEEEIYPNNTVTCNDYTV  
 39 NQEEYGGAYT SRNRGYNEAPSVPADYASVY  
 40 EEKSYTDGRRENPCFNRGYRDYTPLPVGY  
 41 VTKELEYFPETDKVWIEIGETEGTFIVDSV  
 42 ELLLMEE

43 which comprises culturing a prokaryotic microbe  
44 hosting a recombinant DNA transfer vector, denoted  
45 pSYW1, comprising DNA having the following nucleotide  
46 sequence or equivalent nucleotide sequences containing  
47 bases whose translated region codes for the same  
48 amino acid sequence:

		(start	HD-73)	ATG	GATAACAATC	400
49	CGAACATCAA	TGAATGCATT	CCTTATAATT	GTTTAAGTAA	CCCTGAAGTA	
50	GAAGTATTAG	GTGGAGAAAG	AATAGAAACT	GGTTACACCC	CAATCGATAT	500
51	TTCTTTGTCG	CTAACGCAAT	TTCTTTTGAG	TGAATTTGTT	CCCGGTGCTG	
52	GATTTGTGTT	AGGACTAGTT	GATATAATAT	GGGGAAATTT	TGGTCCCTCT	600
53	CAATGGGACG	CATTTCTTGT	ACAAATTGAA	CAGTTAATTA	ACCAAAGAAT	
54	AGAAGAATTC	GCTAGGAACC	AAGCCATTTT	TAGATTAGAA	GGACTAAGCA	700
55	ATCTTTATCA	AATTTACGCA	GAATCTTTTA	GAGAGTGGGA	AGCAGATCCT	
56	ACTAATCCAG	CATTAAGAGA	AGAGATGCGT	ATTCAATTCA	ATGACATGAA	800
57	CAGTGCCTTT	ACAACCGCTA	TTCTCTTTTT	TGCAGTTCAA	AATTATCAAG	
58	TTCTCTTTTT	ATCAGTATAT	GTTCAGCTG	CAAATTTACA	TTTATCAGTT	900
59	TTGAGAGATG	TTTCAGTGTT	TGGACAAAGG	TGGGGATTTG	ATGCCGCGAC	
60	TATCAATAGT	CGTTATAATG	ATTTAACTAG	GCTTATTGGC	AACTATACAG	1000
61	ATTATGCTGT	ACGCTGGTAC	AATACGGGAT	TAGAAGCTGT	ATGGGGACCG	
62	GATTCTAGAG	ATTGGGTAAG	GTATAATCAA	JTTAGAAGAG	AATTAACACT	1100
63	AACTGTATTA	GATATCGTTG	CTCTGTTCCC	GAATTATGAT	AGTAGAAGAT	
64	ATCCAATTCT	AACAGTTTCC	CAATTAACAA	GAGAAATTTA	TACAAACCCA	1200
65	GTATTAGAAA	ATTTTGATGG	TAGTTTTCGA	GGCTCGGCTC	AGGGCATAGA	
66	AGGAAGTATT	AGGAGTCCAC	ATTTGATGGA	TATACTTAAC	AGTATAACCA	1300
67	TCTATACGGA	TGCTCATAAA	GGGGAATATT	ATTGGTCAGG	GCATCAAATA	
68	ATGGCTTCTC	CTGTAGGGTT	TTGGGGGCCA	GAATTCACCT	TTCCGCTATA	1400
69	TGSAACTATG	GGAAATGCAG	CTCCACAACA	ACGTATTGTT	GCTCAACTAG	
70	GTCAGGGCGT	GTATAGAACA	TTATCGTCCA	CTTTATATAG	AAGACCTTTT	1500
71	AATATAGGSA	TAAATAATCA	ACAACATCT	GTTCTTGACG	GGACAGAATT	
72	TGCTTATGSA	ACCTCCTCAA	ATTTGCCATC	CGCTGTATAC	AGAAAAAGCG	1600
73	GAACGGTAGA	TTCGCTGGAT	GAAATACCGC	CACAGAATAA	CAACGTGCCA	
74	CCTAGGCAAG	GATTTAGTCA	TCGATTAAGC	CATGTTTCAA	TGTTTCGTTT	1700
75	AGGCTTTAGT	AATAGTAGTG	TAAGTATAAT	AAGAGCT	(end hd-73)	
76	(start	HD-1)	CCAACGT	TTTCTTGGCA	GCATCGCAST	1900
77	GCTGAATTTA	ATAATATAAT	TCCTTCATCA	CAAATTACAC	AAATACCTTT	
78	AACAAAATCT	ACTAATCTTG	GCTCTGGAAC	TTCTGTCTGT	AAAGGACCAG	2000
79	GATTTACAGG	AGGAGATATT	CTTCGAAGAA	CTTCACCTGG	CCAGATTTCA	
80	ACCTTAAGAG	TAAATATTAC	TGCACCATTA	TCACAAAGAT	ATCGGGTAAG	2100
81	AATTCGCTAC	GCTTCTACTA	CAAATTTACA	ATTCCATACA	TCAATTGACG	
82	GAAGACCTAT	TAATCAGGGT	AATTTTTCAG	CAACTATGAG	TAGTGGGAGT	2200
83	AATTTACAGT	CCGGAAGCTT	TAGGACTGTA	GGTTTTACTA	CTCCGTTTAA	
84	CTTTTCAAAT	GGATCAAGTG	TATTTACGTT	AAGTGCTCAT	GTCTTCAATT	2300
85	CAGGCAATGA	AGTTTATATA	GATCGAATTG	AATTTGTTCC	GGCAGAAGTA	
86	ACCTTTGAGG	CAGATATATG	TTTAGAAAGA	GCACAAAAGT	CGGTGAATGA	2400
87	GCTGTTTACT	TCTTCCAATC	AAATCGGGTT	AAACACAGAT	GTGACGGATT	
88	ATCATATTGA	TCAAGTATCC	AATTTAGTTG	AGTGTTTATC	AGATGAATTT	2500
89	TGTCTGGATG	AAAAACAAGA	ATTGTCCGAG	AAAGTCAAAC	ATGCGAAGCG	
90	ACTTAGTGAT	GAGCGGAATT	TACTTCAAGA	TCCAAACTTC	AGAGGGATCA	2600
91	ATAGACAAC	AGACCGTGGC	TGGAGAGGAA	GTACGGATAT	TACCATCCAA	
92						

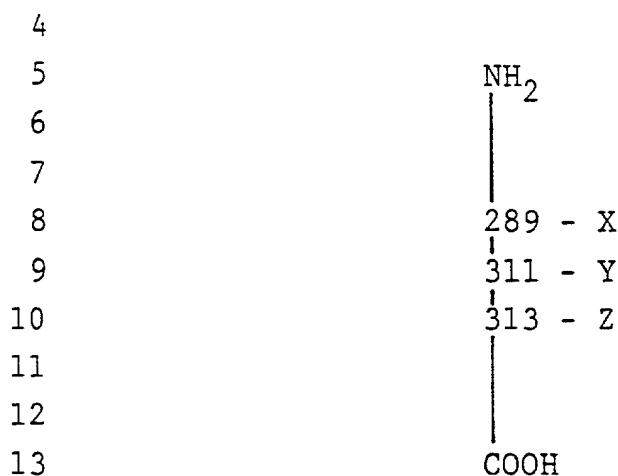
93 GGAGGCGATG ACGTATTCAA AGAGAATTAC GTTACGCTAT TGGGTACCTT 2700  
 94 TGATGAGTGC TATCCAACGT ATTTATATCA AAAAATAGAT GAGTCGAAAT  
 95 TAAAAGCCTA TACCCGTTAT CAATTAAGAG GGTATATCGA AGATAGTCAA 2800  
 96 GACTTAGAAA TCTATTTAAT TCGCTACAAT GCAAAACATG AAACAGTAAA  
 97 TGTGCCAGGT ACGGGTTCCT TATGGCCGCT TTCAGCCCAA AGTCCAATCG 2900  
 98 GAAAGTGTGG AGAGCCGAAT CGATGCGCSC CACACCTTGA ATGGAATCCT  
 99 GACTTAGATT GTTCGTGTAG GGATGGAGAA AAGTGTGCCC ATCATTGCGA 3000  
 100 TCATTTCTCC TTAGACATTG ATGTAGGATG TACAGACTTA AATGAGGACC  
 101 TAGGTGTATG GGTGATCTTT AAGATTAAGA CGCAAGATGG GCACGCAAGA 3100  
 102 CTAGGGAATC TAGAGTTTCT CGAAGAGAAA CCATTAGTAG GAGAAGCGCT  
 103 AGCTCGTGTG AAAAGAGCGG AGAAAAAATG GAGAGACAAA CGTGAAAAAT 3200  
 104 TGAATGGGA AACAAATATC GTTTATAAAG AGGCAAAAGA ATCTGTAGAT  
 105 GCTTTATTTG TAAACTCTCA ATATGATCAA TTACAAGCGG ATACGAATAT 3300  
 105 TGCCATGATT CATGCGGCGAG ATAAACGTGT TCATAGCATT CGAGAAGCTT  
 107 ATCTGCCTGA GCTGTCTGTG ATTCCGGGTG TCAATGCGSC TATTTTTGAA 3400  
 108 GAATTAGAAG GGCCTATTTT CACTGCATTG TCCCTATATG ATGCGAGAAA  
 109 TGTCAATAAA AATGGTGATT TTAATAATGG CTTATCCTGC TGGAADGTGA 3500  
 110 AAGGGCATGT AGATGTAGAA GAACAAAACA ACCAACGTTG GGTCCCTTGT  
 111 CTTCCGGAAT GGGGAAGCAGA AGTGTACACA GAAGTTCTGT TCTGTCCGGG 3600  
 112 TCGTGGCTAT ATCCTTCGTG TCACAGCGTA CAAGGAGGGA TATGGAGAAG  
 113 GTTGCGTAAC CATTGATGAG ATCGAGAACA ATACAGACGA ACTGAAGTTT 3700  
 114 AGCAACTGCG TAGAAGAGGA AATCTATCCA AATAACACGG TAACGTGTAA  
 115 TGATTATACT GTAAATCAAG AAGAATACGG AGGTGCGTAC ACTTCTCGTA 3800  
 116 ATCGAGGATA TAACGAAGCT CCTTCCGTAC CAGCTGATTA TGCCTCAGTC  
 117 TATGAAGAAA AATCGTATAC AGATGGACGA AGAGAGAATC CTTGTGAATT 3900  
 118 TAACAGAGGG TATAGGGATT ACACGCCACT ACCAGTTGGT TATGTGACAA  
 119 AAGAATTAGA ATACTTCCCA GAAACCGATA AGGTATGGAT TGAGATTGGA 4000  
 120 GAAACGGAAG GAACATTTAT CGTGGACAGC GTGGAATTAC TCCTTATGGA  
 121 GGAA (end HD-1).

51. A chimeric toxin, having the amino acid  
 sequence of toxin EW3, with changes which can be shown  
 schematically as follows:



13 wherein X is one of the 20 common amino acids  
14 except Asp when the amino acid at position 425 is  
15 Gly; Y is one of the 20 common amino acids except  
16 Gly when the amino acid at position 411 is Asp.

1 52. A chimeric toxin, having the amino acid  
2 sequence of toxin EW3, with changes which can be shown  
3 schematically as follows:



15 wherein X is one of the 20 common amino acids except  
16 Arg when the amino acid at position 311 is Arg and the  
17 amino acid at position 313 is Tyr; Y is one of the 20  
18 common amino acids except Arg when the amino acid at  
19 position 289 is Arg and the amino acid at position 313  
20 is Tyr; and Z is one of the 20 common amino acids  
21 except Tyr when the amino acid at position 289 is  
22 Arg and the amino acid at position 311 is Arg.

1 53. DNA encoding a chimeric toxin as shown in  
2 claim 51.

1 54. DNA encoding a chimeric toxin as-shown in  
2 claim 52.

1           55. A recombinant DNA transfer vector comprising  
2 DNA encoding a chimeric toxin as shown in claim 51.

1           56. A recombinant DNA transfer vector comprising  
2 DNA encoding a chimeric toxin as shown in claim 52.

1           57. A chimeric toxin comprising the variable  
2 region or regions of two or more Bacillus toxins.

1           58. A toxin, according to claim 57, wherein the  
2 Bacillus toxins are B. thuringiensis toxins.

1           59. A toxin, according to claim 58, wherein the  
2 B. thuringiensis toxins are B. thuringiensis var.  
3 kurstaki HD-1 toxin and B. thuringiensis var. kurstaki  
4 HD-73 toxin.

1           60. A toxin, according to claim 58, wherein  
2 the B. thuringiensis toxins are encoded by a pesticide-  
3 producing strain of Bacillus thuringiensis, consisting  
4 of B. thuringiensis M-7, B. thuringiensis var. kurstaki,  
5 B. thuringiensis var. finitimus, B. thuringiensis var.  
6 alesti, B. thuringiensis var. sotto, B. thuringiensis  
7 var. dendrolimus, B. thuringiensis var. kenyae, B.  
8 thuringiensis var. galleriae, B. thuringiensis var.  
9 canadensis, B. thuringiensis var. entomocidus, B.  
10 thuringiensis var. subtoxicus, B. thuringiensis var.  
11 aizawai, B. thuringiensis var. morrisoni, B. thuringiensis  
12 var. ostrinae, B. thuringiensis var. tolworthi, B.  
13 thuringiensis var. darmstadiensis, B. thuringiensis  
14 var. toumanoffi, B. thuringiensis var. kyushuensis, B.  
15 thuringiensis var. thompsoni, B. thuringiensis var.  
16 pakistani, B. thuringiensis var. israelensis, B. thurin-  
17 giensis var. indiana, B. thuringiensis var. dakota,



18 B. thuringiensis var. tohokuensis, B. thuringiensis  
19 var. kumanotoensis, B. thuringiensis var. tochigiensis,  
20 B. thuringiensis var. colmeri, B. thuringiensis var.  
21 wuhanensis, B. thuringiensis var. tenebrionis, B.  
22 thuringiensis var. thuringiensis, and other Bacillus  
23 species selected from B. cereus, B. moritai, B.  
24 popilliae, B. lentimorbus, and B. sphaericus.